

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 16:01:57 : Search time 97146 Seconds
(without alignments)
17846.554 Million cell updates/sec

Title: US-09-728-552A-3_COPY_1_40000

Perfect score: 40000

Sequence: 1 gaattctcgtcgtcagcct.....tttgggtatttagattctta 40000

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*
2: gb.htg.*
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4: gb.om.*
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6: gb.pat.*
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8: gb.pl.*
9: gb.pr.*
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15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
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32: em.htg.other.*
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41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40000	100.0	40917	6	AX033911	AX033911 Sequence
2	39963	99.9	80622	9	AF222855	AF222855 Homo sapi
3	39244.8	98.1	112442	9	AL355340	AL355340 Human DNA
4	38866.2	97.2	69058	9	AF222856	AF222856 Homo sapi
5	38866.2	97.2	80202	9	AF222854	AF222854 Homo sapi
6	38782.8	97.0	41008	6	AX033912	AX033912 Sequence
7	38746.6	96.9	80155	2	AF042484	AF042484 Homo sapi
8	30556.6	76.4	176432	2	AL391648	AL391648 Homo sapi
9	5429.6	13.6	11841	2	U82209	U82209 Homo sapien
10	1471.6	3.7	2418	9	HSU49973	U49973 Human Tigge
11	1206.4	3.0	100020	9	AC092165	AC092165 Homo sapi
12	1206.4	3.0	158276	2	AC012033	AC012033 Homo sapi
13	1206.4	3.0	179816	2	AC074188	AC074188 Homo sapi
14	1204.8	3.0	2641	9	BC035143	BC035143 Homo sapi
15	1182.8	3.0	51343	9	AC108017	AC108017 Homo sapi
16	1161	2.9	2545	9	BC063500	BC063500 Homo sapi
17	1160.6	2.9	2448	6	AX714168	AX714168 Sequence
18	1160.6	2.9	2448	9	AK056329	AK056329 Homo sapi
19	1127.6	2.8	46851	9	AL136168	AL136168 Human DNA
20	1127.6	2.8	189210	9	AC018719	AC018719 Homo sapi
21	1122.8	2.8	214175	9	CNS01DRT	AL118557 Human chr
22	1118.6	2.8	122001	9	AP003168	AP003168 Homo sapi
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24	1118.6	2.8	160452	2	AC040946	AC040946 Homo sapi
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34	1105.6	2.8	200853	9	CNS01DSQ	AL121839 Human chr
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36	1085.2	2.7	143823	9	AC019195	AC019195 Homo sapi
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44	1072	2.7	211156	2	AC136939	AC136939 Homo sapi
45	1071	2.7	138350	2	AC010801	AC010801 Homo sapi

ALIGNMENTS

RESULT 1
AX033911
LOCUS AX033911 40917 bp DNA linear PAT 21-SEP-2000
DEFINITION Sequence 3 from Patent WO9851790.
ACCESSION AX033911
VERSION AX033911.1 GI:10280479
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1
AUTHORS Cancilla.M.R., Choo,K.H. and Du,S.D.
TITLE A novel nucleic acid molecule
JOURNAL Patent: WO 9851790-A 3 19-NOV-1998;
CANCILLA MICHAEL ROBERT (AU) ; CHOO KONG HONG ANDY (AU) ; SART

Pred. No. is the number of results predicted by chance to have a

DESIRE DU (AU) : AMRAD OPERATIONS PTY LTD (AU)

FEATURES
source

Location/Qualifiers

1. 40917

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 40000; DB 6; Length 40917;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GAATTCCTCCCTCAGCTCCCAAGTAGCTCAGGTTACAGGTGCGAGCCACCAAGTCCA 60

QY 61 GCTAATTTTGTATTTTAGTAGAGCGGGTTTACCGTGTGTTGCGAGCTGGTATCAAA 120
DB 61 GCTAATTTTGTATTTTAGTAGAGCGGGTTTACCGTGTGTTGCGAGCTGGTATCAAA 120

QY 121 CTCTGACCTCAAGTGATCTGCTGCTCAGCTCCCAAAATGCTAGGATTACAGGTG 180
DB 121 CTCTGACCTCAAGTGATCTGCTGCTCAGCTCCCAAAATGCTAGGATTACAGGTG 180

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DB 181 AGTCACGACCGAGCGCCCTTCTTCACTATCACTCTTTTGTCTATTTTGTATGATG 240

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DB 241 AGCTTTATTTATTTAGGGGCACATATTTAAATTTTATGCTCTTATGATAGATGACT 300

QY 301 GTCATTTATGAATCTCTGTATTCATCTCCCTGATAGTATTTCTTTTCTAAATTTTTCG 360
DB 301 GTCATTTATGAATCTCTGTATTCATCTCCCTGATAGTATTTCTTTTCTAAATTTTTCG 360

QY 361 AATGTGCTCTATTTACATAGCACCTCTGGCTTTTAAATTTATGATTTTATGGTATA 420
DB 361 AATGTGCTCTATTTACATAGCACCTCTGGCTTTTAAATTTATGATTTTATGGTATA 420

QY 421 TATTTTCTCTTTTCTTTTAAAGTTTATGATTTATGTTTCTCTTATCTAATAAGTGG 480
DB 421 TATTTTCTCTTTTCTTTTAAAGTTTATGATTTATGTTTCTCTTATCTAATAAGTGG 480

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DB 481 GTGTCTTATAGGAGAGATATCTGGCTGTGATGATTTATTTATCTGATTAATCTCAAC 540

QY 541 CTTTTTGTGGAGTGTATAGGCCATTTACATTTAGTGTAAATATAGACATGGTTGATTT 600
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DB 781 TTTAACTTATCACGATTTACCTTCAATATAGTATTTTACCGCTCAAGTGTAAATCTAGAAC 840

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DB 841 CTTTACAGAGTATATTTTCTCTCTCTAAATTTTATGCTATGCTATTAATACATT 900

QY 901 AGGTTTGTGTTGTTTGTATTTTACCTATTTGCTGTGGCTGGGCTCAGCAAAATTTTCT 960

DB 901 AGGTTTGTGTTGTTTGTATTTTACCTATTTGCTGTGGCTGGGCTCAGCAAAATTTTCT 960

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QY 1141 ATAGTGTATGTTCTAAAAAACAACATACCTTAATTTTAAAAATGCTTTTATTTACTAAAAAT 1200

DB 1141 ATAGTGTATGTTCTAAAAAACAACATACCTTAATTTTAAAAATGCTTTTATTTACTAAAAAT 1200

QY 1201 GCTAACAAATCATTTGAGCATTCAGTGAGTGTAAATCTTTTGTCTGTGGAAGTCTTTTC 1260

DB 1201 GCTAACAAATCATTTGAGCATTCAGTGAGTGTAAATCTTTTGTCTGTGGAAGTCTTTTC 1260

QY 1261 TTATTGATGACTGATCGGGGTCAGGTGCTGAAGCTTAGGCTGGCTGTGGCAGTTTCTTA 1320

DB 1261 TTATTGATGACTGATCGGGGTCAGGTGCTGAAGCTTAGGCTGGCTGTGGCAGTTTCTTA 1320

QY 1321 AAACAACAGTGAAGATTGCAATATCAGTTGACTCTTCTTTTCAATGAAGATTTCCTCTTA 1380

DB 1321 AAACAACAGTGAAGATTGCAATATCAGTTGACTCTTCTTTTCAATGAAGATTTCCTCTTA 1380

QY 1381 GTGTGATGCTTTTGTATAGCATTTTATGCAAGTAGAATCTTTTGAATTTGATCA 1440

DB 1381 GTGTGATGCTTTTGTATAGCATTTTATGCAAGTAGAATCTTTTGAATTTGATCA 1440

QY 1441 ATCTCTCTCAAACTCTGCTCTGCTTTAAACAACCTTAAGTAAATAATATTAATCTGAATCCATT 1500

DB 1441 ATCTCTCTCAAACTCTGCTCTGCTTTAAACAACCTTAAGTAAATAATATTAATCTGAATCCATT 1500

QY 1501 GTGTGCAATTTCAACAATTTTACAGTGCTTTACCAGGAGTAGATTCATCTCATTTCTCT 1560

DB 1501 GTGTGCAATTTCAACAATTTTACAGTGCTTTACCAGGAGTAGATTCATCTCATTTCTCT 1560

QY 1561 GAGATGAATCTTTGCTCATCCATTAAGAGAAATCTCTCATCTGTTCAAGTTTATCAIG 1620

DB 1561 GAGATGAATCTTTGCTCATCCATTAAGAGAAATCTCTCATCTGTTCAAGTTTATCAIG 1620

QY 1621 AGATTGAGCAATACAGTCACTTTTCAAGCTCAGCTTCACTTTTAAATTTTCAAGTCTCTTT 1680

DB 1621 AGATTGAGCAATACAGTCACTTTTCAAGCTCAGCTTCACTTTTAAATTTTCAAGTCTCTTT 1680

QY 1681 GCTGTTTCTACCACTCTGTTCTCTCTCTCATTTGAAGCTCTTGAACCTCTCCAAGTCA 1740

DB 1681 GCTGTTTCTACCACTCTGTTCTCTCTCTCATTTGAAGCTCTTGAACCTCTCCAAGTCA 1740

QY 1741 TCCATGAGGGTTGGAATTCGACTTCTTCCAAATTTCTGTTAATTTATATTTTGAAGCTCC 1800

DB 1741 TCCATGAGGGTTGGAATTCGACTTCTTCCAAATTTCTGTTAATTTATATTTTGAAGCTCC 1800

QY 1801 CATGAATCATGAATTTCTTTAATGGACCTGGATGGTGAATCTTTTCCAAAGGTTTTC 1860

DB 1801 CATGAATCATGAATTTCTTTAATGGACCTGGATGGTGAATCTTTTCCAAAGGTTTTC 1860

QY 1861 AATTTACTTGTAGTCCAGATCCATCCATCCAGAGGATCCACTTTCAATGCCAGTTTATAGCCT 1920

DB 1861 AATTTACTTGTAGTCCAGATCCATCCATCCAGAGGATCCACTTTCAATGCCAGTTTATAGCCT 1920

QY 1921 TATGGAATGATTTTCTTCAATATAAGGCTTGAAGTTGAAATTTACTCTTTGATTCATTT 1980

DB 1921 TATGGAATGATTTTCTTCAATATAAGGCTTGAAGTTGAAATTTACTCTTTGATTCATTT 1980

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2221 Db TGTAGCATAAATCTTAAGGAGCTTAGGATTTTCAAGATGGTAAATGAAATGGCATCAA 2280
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14581 ACCATGCTGGCCAGAGACACTTTTGGAGTGAAGAGAACTGAGAAATTAATCACTGA 14640
14641 TCTTAACTGGGACCAATCCAGGCAAGCAGATGCCATTTACCACTAGCTAGAAAGCTTCG 14700
14641 TCTTAACTGGGACCAATCCAGGCAAGCAGATGCCATTTACCACTAGCTAGAAAGCTTCG 14700
14701 CAAGGCTCATTTACCTTGGTATATAGCAAAATCTTTTGAATTTCTGAAATTTCTGTT 14760
14701 CAAGGCTCATTTACCTTGGTATATAGCAAAATCTTTTGAATTTCTGAAATTTCTGTT 14760
14761 AAGTCATTGAGTGTGCTGTCAGAGGCAATATGGTAGAATTTCTAATTTTCAGGCA 14820
14761 AAGTCATTGAGTGTGCTGTCAGAGGCAATATGGTAGAATTTCTAATTTTCAGGCA 14820
14821 GACAAACACTTTCTGCTGATTTGTAGCAGGTAAGAGGAGTCAAGGCAAGAAACCAAC 14880
14821 GACAAACACTTTCTGCTGATTTGTAGCAGGTAAGAGGAGTCAAGGCAAGAAACCAAC 14880
14881 TGGAGCTCGAAGAGGCAATAACGTCCTAATGCACCTGATGATGATGTTAAATGTT 14940
14881 TGGAGCTCGAAGAGGCAATAACGTCCTAATGCACCTGATGATGATGTTAAATGTT 14940
14941 ATCAGCTTAAAGATCTTTTCAATAAATAAACTTATCATTTTGGAGGCGCACAGAAATCG 15000
14941 ATCAGCTTAAAGATCTTTTCAATAAATAAACTTATCATTTTGGAGGCGCACAGAAATCG 15000
15001 TGGAAAGCTGGGATTCAGGTTGCTGCTGCTTAAATTTCTGGAATTCAGAAATTAAGTCAA 15060
15001 TGGAAAGCTGGGATTCAGGTTGCTGCTGCTTAAATTTCTGGAATTCAGAAATTAAGTCAA 15060
15061 GGATATCAGTCTAAGTAAGTTTCAATGTTTATATGCCAAGATGAGTGTCTCTAT 15120
15061 GGATATCAGTCTAAGTAAGTTTCAATGTTTATATGCCAAGATGAGTGTCTCTAT 15120
15121 TTTCACTTCAGTAATTCCTCTGAATTAATACACCTTAAAAATAGCTCAGCTTCTCAA 15180

Db	15121	TTTCACCTCCAGTAATTCCTTCTGAATTAATACACCTTAAATAATAGCTGCAGCTTCTCAA	15180
Qy	15181	ATCTGTGAGAACTGCTATGCTGCTGCTACACTTTCTTTTCCGGAAGGCTTTTGAGG	15240
Db	15181	ATCTGTGAGAACTGCTATGCTGCTGCTACACTTTCTTTTCCGGAAGGCTTTTGAGG	15240
Qy	15241	TCCTTCAAGAACTCAATTCAAATTCAGCAACAATTAGGGGCTCTAAGGTATACAGACGCTG	15300
Db	15241	TCCTTCAAGAACTCAATTCAAATTCAGCAACAATTAGGGGCTCTAAGGTATACAGACGCTG	15300
Qy	15301	TGCAAGATGCTCTGAGACACAAAGAGGAGGCTCAAGCCCTGCTTCAAGGACCTCTCTA	15360
Db	15301	TGCAAGATGCTCTGAGACACAAAGAGGAGGCTCAAGCCCTGCTTCAAGGACCTCTCTA	15360
Qy	15361	TAATATAGGAGGAGAAAGAGAAACACTAATACACATAGGTAGGTGCAATTAAGAGG	15420
Db	15361	TAATATAGGAGGAGAAAGAGAAACACTAATACACATAGGTAGGTGCAATTAAGAGG	15420
Qy	15421	TACATACATTAAGCCAGGTGCTAGGTGTAAGAGATTTGTAACATGAGAAATTTCTGCA	15480
Db	15421	TACATACATTAAGCCAGGTGCTAGGTGTAAGAGATTTGTAACATGAGAAATTTCTGCA	15480
Qy	15481	TGTTTGAATATCTTATAATTTTAAATAATTAATAATGGAGATACATATATATATTTA	15540
Db	15481	TGTTTGAATATCTTATAATTTTAAATAATTAATAATGGAGATACATATATATATTTA	15540
Qy	15541	TGTATGTATATATGTAATGTAATACACATATATACATATAATATATATATATATG	15600
Db	15541	TGTATGTATATATGTAATGTAATACACATATATACATATAATATATATATATATG	15600
Qy	15601	TATATATGTATATAGACATAAATATGTAATATATGTAATATATACATATAATATGTA	15660
Db	15601	TATATATGTATATAGACATAAATATGTAATATATGTAATATATACATATAATATGTA	15660
Qy	15661	TATGTCTATATAGACATAAATATGTAATATATGTAATATAGACATAAATATGTAATATG	15720
Db	15661	TATGTCTATATAGACATAAATATGTAATATATGTAATATAGACATAAATATGTAATATG	15720
Qy	15721	TGTAATAGACATAAATATGTAATATGTAATATAGACATAAATATGTAATATGTA	15780
Db	15721	TGTAATAGACATAAATATGTAATATGTAATATAGACATAAATATGTAATATGTA	15780
Qy	15781	TATAGACATAAATATGTAATATGTAATATAGACATAAATATGTAATATGTAATATA	15840
Db	15781	TATAGACATAAATATGTAATATGTAATATAGACATAAATATGTAATATGTAATATA	15840
Qy	15841	GACATAAATATGTAATATGTAATATAGACATAAATATGTAATATGTAATATAGACA	15900
Db	15841	GACATAAATATGTAATATGTAATATAGACATAAATATGTAATATGTAATATAGACA	15900
Qy	15901	TAAATATGTAATATGTAATATAGACATAAATATGTAATATGTAATATAGACATAAA	15960
Db	15901	TAAATATGTAATATGTAATATAGACATAAATATGTAATATGTAATATAGACATAAA	15960
Qy	15961	TATGTAATATGTAATATAGACATAAATATGTAATATGTAATATAGACATAAATATG	16020
Db	15961	TATGTAATATGTAATATAGACATAAATATGTAATATGTAATATAGACATAAATATG	16020
Qy	16021	TATATATGTAATATAGACATAAATATGTAATATGTAATATAGACATAAATATGTA	16080
Db	16021	TATATATGTAATATAGACATAAATATGTAATATGTAATATAGACATAAATATGTA	16080
Qy	16081	TATACACATATATACATACATAAATCTTGCATTAATACCATTCACCTTGAACCCAT	16140
Db	16081	TATACACATATATACATACATAAATCTTGCATTAATACCATTCACCTTGAACCCAT	16140
Qy	16141	CTTCCCTAAACCTGCTCATAAAGAGTCTCTTTTCCCTGTACCTATGCAATGTAAAGT	16200
Db	16141	CTTCCCTAAACCTGCTCATAAAGAGTCTCTTTTCCCTGTACCTATGCAATGTAAAGT	16200
Qy	16201	AGCAAAACACATCTTTTGGGTCCCAATACATTCCTGCTAGTTTGGCCCTTAAACAGTC	16260
Db	16201	AGCAAAACACATCTTTTGGGTCCCAATACATTCCTGCTAGTTTGGCCCTTAAACAGTC	16260
Qy	16261	TTTCATGTGAAATTTTACTGTTTCTGCTTAACTTGCCTGCTGCTGCGCTACATGAGATTTT	16320
Db	16261	TTTCATGTGAAATTTTACTGTTTCTGCTTAACTTGCCTGCTGCTGCGCTACATGAGATTTT	16320
Qy	16321	GGCTCTGGCTCTCTGCTGCTGCTTCAACCCCTGCTTCCGCAAGAAATCTGCTATGCT	16380
Db	16321	GGCTCTGGCTCTCTGCTGCTGCTTCAACCCCTGCTTCCGCAAGAAATCTGCTATGCT	16380
Qy	16381	GACCACTGCTCATCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	16440
Db	16381	GACCACTGCTCATCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	16440
Qy	16441	TGGAATCTCTCTGGGGAGTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	16500
Db	16441	TGGAATCTCTCTGGGGAGTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	16500
Qy	16501	ATAGGTAAAGTGAAGTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	16560
Db	16501	ATAGGTAAAGTGAAGTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	16560
Qy	16561	CTTCTGACATGCTGGGCTTGAACGGGTCTGGATATCCGATGGATGGCCCTTAAAGCTGAG	16620
Db	16561	CTTCTGACATGCTGGGCTTGAACGGGTCTGGATATCCGATGGATGGCCCTTAAAGCTGAG	16620
Qy	16621	CTCAAGGCTTAAAGGAGAGATAGGGGCTGATGATCTGAGATTTCAATAGTGTGGCTGAT	16680
Db	16621	CTCAAGGCTTAAAGGAGAGATAGGGGCTGATGATCTGAGATTTCAATAGTGTGGCTGAT	16680
Qy	16681	GTTTTAAACCCAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	16740
Db	16681	GTTTTAAACCCAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	16740
Qy	16741	AAATGGCTTCTGGGCTCTTCTAGTCAATCAAAATCGGACCTCTGAGGAGGAGGAGGAGG	16800
Db	16741	AAATGGCTTCTGGGCTCTTCTAGTCAATCAAAATCGGACCTCTGAGGAGGAGGAGGAGG	16800
Qy	16801	GAAAGGTAGATCTCTGGGCTCACGGGATTAAGAGCTTTTCAAAAGTGGGGCTGGCCAG	16860
Db	16801	GAAAGGTAGATCTCTGGGCTCACGGGATTAAGAGCTTTTCAAAAGTGGGGCTGGCCAG	16860
Qy	16861	TGCTGTCTGAAAGGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	16920
Db	16861	TGCTGTCTGAAAGGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	16920
Qy	16921	GAAATTTGAAATTTTAAAGTCTGTAACCTTAAAGAGCAATTTTAGATACCTTTTGAAT	16980
Db	16921	GAAATTTGAAATTTTAAAGTCTGTAACCTTAAAGAGCAATTTTAGATACCTTTTGAAT	16980
Qy	16981	TATTTGCAAGATTTTGGTGTATGTTTATTTCCAGGCAAGGAGGAGGAGGAGGAGG	17040
Db	16981	TATTTGCAAGATTTTGGTGTATGTTTATTTCCAGGCAAGGAGGAGGAGGAGGAGG	17040
Qy	17041	AATCTTACTGAAACAGTTACTGCAATGCTGCACTGTAAACCTGTTTAAATTTCTACGG	17100
Db	17041	AATCTTACTGAAACAGTTACTGCAATGCTGCACTGTAAACCTGTTTAAATTTCTACGG	17100
Qy	17101	CAACCTTATAGAGTGTGCTCATCCCATCTTACAGATGAGGATATGAGGTGCAAGCT	17160
Db	17101	CAACCTTATAGAGTGTGCTCATCCCATCTTACAGATGAGGATATGAGGTGCAAGCT	17160
Qy	17161	AGATTAAGAGCTTTGGCTCAGGTTTACACCACTGGTTAACTGAGCTAGGATTTGAACC	17220
Db	17161	AGATTAAGAGCTTTGGCTCAGGTTTACACCACTGGTTAACTGAGCTAGGATTTGAACC	17220
Qy	17221	CGGATGGGCTGATCCAGAGCTCATGCTTTAAATCGCTAGACTGGTCTCACAGAGACT	17280
Db	17221	CGGATGGGCTGATCCAGAGCTCATGCTTTAAATCGCTAGACTGGTCTCACAGAGACT	17280
Qy	17281	GGGACCCGAAATAATTAATAAATAAATAAGGAGGAGGAGGAGGAGGAGGAGGAGG	17340
Db	17281	GGGACCCGAAATAATTAATAAATAAATAAGGAGGAGGAGGAGGAGGAGGAGGAGG	17340

[illegible]

Db	23881	TTAGTTGCTTAGGAAAAATACAAACACACACACTTTAAATATATATATAAAATCCCGTCT	23940
Qy	23941	AAACCTCAGAGTCCAGAACCGCATCTCTAACTCATGTCTATGCATATATATTTAAATTTTT	24000
Db	23941	AAACCTCAGAGTCCAGAACCGCATCTCTAACTCATGTCTATGCATATATATTTAAATTTTT	24000
Qy	24001	GTCTTTTAAAACTACAAATAGGATGTATTAATAGTTCCCAATCAATGTCTAGTTAG	24060
Db	24001	GTCTTTTAAAACTACAAATAGGATGTATTAATAGTTCCCAATCAATGTCTAGTTAG	24060
Qy	24061	CCGAGGAAAGATPAGCATAGTTAAAGACTTAAATGGCTTTTACAACATATATCAAAAGGA	24120
Db	24061	CCGAGGAAAGATPAGCATAGTTAAAGACTTAAATGGCTTTTACAACATATATCAAAAGGA	24120
Qy	24121	CAAAATAAGGGAAACAGAGTCTAGAAATGAGGAACTGGGACACAGGCAAAAATAAAAA	24180
Db	24121	CAAAATAAGGGAAACAGAGTCTAGAAATGAGGAACTGGGACACAGGCAAAAATAAAAA	24180
Qy	24181	TGAGAACTGGGACATGAATAAACCAAGGGATAGACTAATACAAAAACACCCCAATAA	24240
Db	24181	TGAGAACTGGGACATGAATAAACCAAGGGATAGACTAATACAAAAACACCCCAATAA	24240
Qy	24241	ATAGCCAGCATTTGCTGAGCTCTTACTGTAGGCTGTTCTTAAGCACTTTACATATATTA	24300
Db	24241	ATAGCCAGCATTTGCTGAGCTCTTACTGTAGGCTGTTCTTAAGCACTTTACATATATTA	24300
Qy	24301	CTCATTTTCATCTCAAGGAACCATCTGAGCGACCTGTATCATCTCCATTTTACAGA	24360
Db	24301	CTCATTTTCATCTCAAGGAACCATCTGAGCGACCTGTATCATCTCCATTTTACAGA	24360
Qy	24361	TAAAGGAATAGACCCAGAGGCTGAGCAACTGGGCTTATTCACAGCTACTATGTTGGAG	24420
Db	24361	TAAAGGAATAGACCCAGAGGCTGAGCAACTGGGCTTATTCACAGCTACTATGTTGGAG	24420
Qy	24421	ATGAGATTTAAATCTTAATCATTTGGCTCCAGAGCCCATGACCAATGGCTGGACCTAAGTG	24480
Db	24421	ATGAGATTTAAATCTTAATCATTTGGCTCCAGAGCCCATGACCAATGGCTGGACCTAAGTG	24480
Qy	24481	AATGCATGCGCTATCAACGTTGCAAAAGTGGCCACAGCTCGGATCTCGTTTCCAGT	24540
Db	24481	AATGCATGCGCTATCAACGTTGCAAAAGTGGCCACAGCTCGGATCTCGTTTCCAGT	24540
Qy	24541	AGCCAAAGCAGAGTGTGATCAGACTCTACTTTAATAGCAAGTCTCAGCCAGAGAGA	24600
Db	24541	AGCCAAAGCAGAGTGTGATCAGACTCTACTTTAATAGCAAGTCTCAGCCAGAGAGA	24600
Qy	24601	GGTGGTATCAGGAGCAAAACAGGCTGCTAGTGGAAATCCCACTTCTCTGAGTGGTCC	24660
Db	24601	GGTGGTATCAGGAGCAAAACAGGCTGCTAGTGGAAATCCCACTTCTCTGAGTGGTCC	24660
Qy	24661	ATACAGTTTACTCTACTCTTACAGAAATGAAATAGCTGGAGTTTCAGGTGCGCTTCA	24720
Db	24661	ATACAGTTTACTCTACTCTTACAGAAATGAAATAGCTGGAGTTTCAGGTGCGCTTCA	24720
Qy	24721	ATGCCCTGTTGTCAGGATGGGCTTTTCAAGTTTATTTTTGTTGTTTAAATAGAC	24780
Db	24721	ATGCCCTGTTGTCAGGATGGGCTTTTCAAGTTTATTTTTGTTGTTTAAATAGAC	24780
Qy	24781	TGTACTTTTAAAGAAATTTTATGATTTACAGAAAGATTTGAGAGATAGTACAGAGGTTT	24840
Db	24781	TGTACTTTTAAAGAAATTTTATGATTTACAGAAAGATTTGAGAGATAGTACAGAGGTTT	24840
Qy	24841	CCGTATACCTCACCCAGTTTCTGCAATTTAACTCTTATATTCATTCGCGTACATTT	24900
Db	24841	CCGTATACCTCACCCAGTTTCTGCAATTTAACTCTTATATTCATTCGCGTACATTT	24900
Qy	24901	GTTTACAATTAATGAGCCAGGCGCGCGGACAGTGGTTTCAGGCCCTTAATCCACAGCAC	24960
Db	24901	GTTTACAATTAATGAGCCAGGCGCGCGGACAGTGGTTTCAGGCCCTTAATCCACAGCAC	24960
Qy	24961	TTTGGGAGGAGGCAAGCAATCACTTGAGGTTCAGAGTTCGAGCTAGCCTGACCAA	25020
Db	24961	TTTGGGAGGAGGCAAGCAATCACTTGAGGTTCAGAGTTCGAGCTAGCCTGACCAA	25020
Qy	25021	CATCGTAAACCCCTTCTGTACTAAAAATACAAAAATTTAGCCAGGCATGCTGCTGTTGC	25080
Db	25021	CATCGTAAACCCCTTCTGTACTAAAAATACAAAAATTTAGCCAGGCATGCTGCTGTTGC	25080
Qy	25081	CTGTATTTCCAGATACTCAGGAGCTCAGGACCAAGAAATTTGCTTGAACCGAGGAGCGGA	25140
Db	25081	CTGTATTTCCAGATACTCAGGAGCTCAGGACCAAGAAATTTGCTTGAACCGAGGAGCGGA	25140
Qy	25141	GGTTGCGATAGCCGAGATGTGTCACCTGCACCTCCAGCCTGGGCAACAGAGCGAGATCC	25200
Db	25141	GGTTGCGATAGCCGAGATGTGTCACCTGCACCTCCAGCCTGGGCAACAGAGCGAGATCC	25200
Qy	25201	ATCAAAAAAATAAAAAAAGAAAGAAAGAAAGAAAGAAATTAATAGCCCAATA	25260
Db	25201	ATCAAAAAAATAAAAAAAGAAAGAAAGAAAGAAAGAAATTAATAGCCCAATA	25260
Qy	25261	TTGAGACATTAATTAATAAAGTCCATGTCTTATGAGATTTTCTTAGTGTTCCTGCTGC	25320
Db	25261	TTGAGACATTAATTAATAAAGTCCATGTCTTATGAGATTTTCTTAGTGTTCCTGCTGC	25320
Qy	25321	TGTCAATTTTTCAGTTCCAGGAATGCATTGAGGATGCCATACCAATTTAGTCTCATATC	25380
Db	25321	TGTCAATTTTTCAGTTCCAGGAATGCATTGAGGATGCCATACCAATTTAGTCTCATATC	25380
Qy	25381	TGCTTAGGCTCCTCTTGCTAGACTGAGTTTAAATCTACTTTTCTGAGAGCTCAGAACT	25440
Db	25381	TGCTTAGGCTCCTCTTGCTAGACTGAGTTTAAATCTACTTTTCTGAGAGCTCAGAACT	25440
Qy	25441	TTAGCATTAATTTCTTGGAAATTTACAGTCAATTTTCAAGCACTTATACAAACAGCT	25500
Db	25441	TTAGCATTAATTTCTTGGAAATTTACAGTCAATTTTCAAGCACTTATACAAACAGCT	25500
Qy	25501	AATGTTAGCTTGGCCCAATAACAGTGTTCAGAGTAAATAAATCTTCTTGTGCTGCG	25560
Db	25501	AATGTTAGCTTGGCCCAATAACAGTGTTCAGAGTAAATAAATCTTCTTGTGCTGCG	25560
Qy	25561	ATTGAAAGAACTGCTGTAGCTCTCCAGAGATGATGAATGGGTACACACAGGATTTT	25620
Db	25561	ATTGAAAGAACTGCTGTAGCTCTCCAGAGATGATGAATGGGTACACACAGGATTTT	25620
Qy	25621	TTCCAGGTAAAGCAATTTCTGTGCACTTTCTTAAGCTGACGCTTATATGCAATAATGT	25680
Db	25621	TTCCAGGTAAAGCAATTTCTGTGCACTTTCTTAAGCTGACGCTTATATGCAATAATGT	25680
Qy	25681	CCATTTACAAGACTTATGTTCCGAATTTTCAAGCACTGTTTTCACATAACCTTTCA	25740
Db	25681	CCATTTACAAGACTTATGTTCCGAATTTTCAAGCACTGTTTTCACATAACCTTTCA	25740
Qy	25741	ACTTTGATAGTACTGCTTTTAACTCAAGAAATTTAACTGACTAATTTTTTTTTCAC	25800
Db	25741	ACTTTGATAGTACTGCTTTTAACTCAAGAAATTTAACTGACTAATTTTTTTTTCAC	25800
Qy	25801	CATCAGTTTTTTTCTGTGTGACTCTTTCTCTCTTTTCTGTGTTGCCAGAAACATGCTCAG	25860
Db	25801	CATCAGTTTTTTTCTGTGTGACTCTTTCTCTCTTTTCTGTGTTGCCAGAAACATGCTCAG	25860
Qy	25861	GATTCCTCAGGCTTTAAAAAATGAAAAATGTTTCTCGCAATCTAGTTACTCTGATTT	25920
Db	25861	GATTCCTCAGGCTTTAAAAAATGAAAAATGTTTCTCGCAATCTAGTTACTCTGATTT	25920
Qy	25921	CTCTGTTTCTGTTTATCGCTGGAATTTCTGAAAGCTTGGTGTATTAGTCTTTTTTCATGC	25980
Db	25921	CTCTGTTTCTGTTTATCGCTGGAATTTCTGAAAGCTTGGTGTATTAGTCTTTTTTCATGC	25980
Qy	25981	TGCTGATAAAGATATACCTGAGCTGGATATTTTAAAGAAAAAGAGGTTTAAATGACT	26040
Db	25981	TGCTGATAAAGATATACCTGAGCTGGATATTTTAAAGAAAAAGAGGTTTAAATGACT	26040
Qy	26041	CACAGTTCCAGTGGCTCAGGAGGCTCACAATCATGTGGAAGCAAAAGGCAATGCTT	26100
Db	26041	CACAGTTCCAGTGGCTCAGGAGGCTCACAATCATGTGGAAGCAAAAGGCAATGCTT	26100

QY 26101 ACATGGCAGCAGCAAGAGAGATGAGAACCAAGGATTTCCCTTATATAAACCATCAGA 26160
DB 26101 ACATGGCAGCAGCAAGAGAGATGAGAACCAAGGATTTCCCTTATATAAACCATCAGA 26160
QY 26161 TCTTGTGAGACTTATTCACCTACCAAGAAACAATATGGGTAAACCGCCGCCCATGATTC 26220
DB 26161 TCTTGTGAGACTTATTCACCTACCAAGAAACAATATGGGTAAACCGCCGCCCATGATTC 26220
QY 26221 ATTATCTCCACCGGGCCCTCCACAAACAGTGGGAATTTATGGAGCTACAAATTCAGA 26280
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QY 26401 CCTGAAACTGCTTTTGGAGTAGCTGATAAGTCCAAATATCTGCACCTTTCTCAAT 26460
DB 26401 CCTGAAACTGCTTTTGGAGTAGCTGATAAGTCCAAATATCTGCACCTTTCTCAAT 26460
QY 26461 TCCGTTCTTTATGCTTTGAGCAATTTGACTGTGTTGGTTGGCCCTCTCTTTTAAAGT 26520
DB 26461 TCCGTTCTTTATGCTTTGAGCAATTTGACTGTGTTGGTTGGCCCTCTCTTTTAAAGT 26520
QY 26521 GTCTCTCAGTTGTTTATGACTAAATGATGATTTCTTTTCTCTCTCTCTCTCTCT 26580
DB 26521 GTCTCTCAGTTGTTTATGACTAAATGATGATTTCTTTTCTCTCTCTCTCTCTCT 26580
QY 26581 ATCTTTTAGCTTCCCTTCCCTCCCATCCCTTAAATGCTTTGTTTCCAGAAATCTGC 26640
DB 26581 ATCTTTTAGCTTCCCTTCCCTCCCATCCCTTAAATGCTTTGTTTCCAGAAATCTGC 26640
QY 26641 CTGACCTTTTGACTTCTATGCTGCTGCTCAATTCATCTATGGTCTTTTATACATTTATG 26700
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QY 26701 CATCTGTGCAATTAACCTCTGCTTTCTGTTAAAGTCCAGTCTCCCATTTTCAAAATGCTC 26760
DB 26701 CATCTGTGCAATTAACCTCTGCTTTCTGTTAAAGTCCAGTCTCCCATTTTCAAAATGCTC 26760
QY 26761 CCGAGATTTCCAAATGAGTATCTCCCAATGATTTAAACCTGCTAAATATCTAACACAT 26820
DB 26761 CCGAGATTTCCAAATGAGTATCTCCCAATGATTTAAACCTGCTAAATATCTAACACAT 26820
QY 26821 AATCTTCCCATCAATTCGTTTCTCTTAAGCTTTTGGTTATTTCTGATTTAGACTCTCTGC 26880
DB 26821 AATCTTCCCATCAATTCGTTTCTCTTAAGCTTTTGGTTATTTCTGATTTAGACTCTCTGC 26880
QY 26881 ACTTCTCCAGGAGCCAGACTTAAACCTTGAATTTCTCACCATAACCTCTCTTTTGTG 26940
DB 26881 ACTTCTCCAGGAGCCAGACTTAAACCTTGAATTTCTCACCATAACCTCTCTTTTGTG 26940
QY 26941 TCCCATTAATCAATTTAGTACAGTGTATCAATGATTTCTGACATATCTTTTCTATT 27000
DB 26941 TCCCATTAATCAATTTAGTACAGTGTATCAATGATTTCTGACATATCTTTTCTATT 27000
QY 27001 TCCCTCCCTGCTATGATTCATCTATAGCAAGAGAGTTGGCCCTTTGATCTGTGGTTT 27060
DB 27001 TCCCTCCCTGCTATGATTCATCTATAGCAAGAGAGTTGGCCCTTTGATCTGTGGTTT 27060
QY 27061 CTGATCTCTGGATTCAACCACTTAGTGGAAATATTTGAGAAAGAGAGCTCTATA 27120
DB 27061 CTGATCTCTGGATTCAACCACTTAGTGGAAATATTTGAGAAAGAGAGCTCTATA 27120
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DB 27121 CTGAGTATGAAAAATTTTATTTCTTCTGATTTTCTTAAACATATACAGTATAACACT 27180
QY 27181 ACAGCATTTACCTGTAGCTATGATCTTTAATCTAGAAATGATTTCAAGTACACCAT 27240

DB 27181 ACAGCATTTACCTGTAGCTATGATCTTTAATCTAGAAATGATTTCAAGTACACCAT 27240
QY 27241 TATATATAAGGACTTGAGCAATCTGTGAAGTTTGGTATTTGTGGGCATATCTGGGACAA 27300
DB 27241 TATATATAAGGACTTGAGCAATCTGTGAAGTTTGGTATTTGTGGGCATATCTGGGACAA 27300
QY 27301 TTCCCCCATGATACAGAGGACAACTATATTTACTCAGTGCCTTACTAAATACAGTTGG 27360
DB 27301 TTCCCCCATGATACAGAGGACAACTATATTTACTCAGTGCCTTACTAAATACAGTTGG 27360
QY 27361 CCAATGTCTTTTCTTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 27420
DB 27361 CCAATGTCTTTTCTTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 27420
QY 27421 ATAGTGTGCCAATGCCAGGTGTACCTTCAAGATATTTCTATTCTAATTTTGTCTCTCA 27480
DB 27421 ATAGTGTGCCAATGCCAGGTGTACCTTCAAGATATTTCTATTCTAATTTTGTCTCTCA 27480
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DB 27481 AGCTTAAAAATATTTAAATGGCCAGGCGCAGTGGCTCACACTTGTAAATCCAGCAATTTG 27540
QY 27541 GGAGGCCAAGGGGGGTGTATCACTTGAAGTCCAGAGTTCAGACAGCTGGCCAAACAT 27600
DB 27541 GGAGGCCAAGGGGGGTGTATCACTTGAAGTCCAGAGTTCAGACAGCTGGCCAAACAT 27600
QY 27601 GGCAAAACCTGTCTCTACAAAAAAGTATAAAGTTAAACAGGTGCTGGAGCAATTTGCT 27660
DB 27601 GGCAAAACCTGTCTCTACAAAAAAGTATAAAGTTAAACAGGTGCTGGAGCAATTTGCT 27660
QY 27661 GTGTTCCAGCTACTCAGGAGGTGAGGAGGAAATCACTTTAAATCTGGAGGTGGAGT 27720
DB 27661 GTGTTCCAGCTACTCAGGAGGTGAGGAGGAAATCACTTTAAATCTGGAGGTGGAGT 27720
QY 27721 TTGAGTGTGCGCAGATCTCTCCACTGCTCAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 27780
DB 27721 TTGAGTGTGCGCAGATCTCTCCACTGCTCAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 27780
QY 27781 CTCAAAAACAATAACAAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 27840
DB 27781 CTCAAAAACAATAACAAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 27840
QY 27841 AAATGCAATTTTGGCCAGATGTGGTGGCTCAAACTGTAAATCCCAACACTTTGGGAGC 27900
DB 27841 AAATGCAATTTTGGCCAGATGTGGTGGCTCAAACTGTAAATCCCAACACTTTGGGAGC 27900
QY 27901 TAAGCCAGGAGTTTCGAGAGAGCTGGGATATATAGGAACACACAAATCTCTACAAAAA 27960
DB 27901 TAAGCCAGGAGTTTCGAGAGAGCTGGGATATATAGGAACACACAAATCTCTACAAAAA 27960
QY 27961 AATCCCAAAATTTAGTCCAGCTTATTTCTGCTGTAGTCCAGTATCTAGGAGGCT 28020
DB 27961 AATCCCAAAATTTAGTCCAGCTTATTTCTGCTGTAGTCCAGTATCTAGGAGGCT 28020
QY 28021 GAGCAGGATTTCTCAGCCAGGAGTTCAAGGTTCCGAGCTATGATGGCACAACCTG 28080
DB 28021 GAGCAGGATTTCTCAGCCAGGAGTTCAAGGTTCCGAGCTATGATGGCACAACCTG 28080
QY 28081 CACTCTCATCTTGGGTGACAGCAAGGTCTATCTCTGGAGAAAAAAGAGGCT 28140
DB 28081 CACTCTCATCTTGGGTGACAGCAAGGTCTATCTCTGGAGAAAAAAGAGGCT 28140
QY 28141 ATTTCTTAGGAGGTTCTTCTCTGAGTCTTAAAGGTTCCAGTCTCTTAAAGC 28200
DB 28141 ATTTCTTAGGAGGTTCTTCTCTGAGTCTTAAAGGTTCCAGTCTCTTAAAGC 28200
QY 28201 ATCAGAGTATGTAGTCAATGGGAGGAGCAATTTAGCCAGAGCAGTTGTCTCCATTTG 28260
DB 28201 ATCAGAGTATGTAGTCAATGGGAGGAGCAATTTAGCCAGAGCAGTTGTCTCCATTTG 28260
QY 28261 CATATTTTAAAAAACAAGCTATAAAAAAGTTGAAAACTACTACGTTCATC 28320

Db	28261	CATATTAAATTTTAAAAAAACAAGCTATATAAAAAAAGTTGAAAACTACTAGTTAGCATC	28320
Qy	28321	AGCCTGACATTTAATGGCCTCGTAATCAAAACCTTTAAATTGACTTTTATAGCCAGTTATGCT	28380
Db	28321	AGCCTGACATTTAATGGCCTCGTAATCAAAACCTTTAAATTGACTTTTATAGCCAGTTATGCT	28380
Qy	28381	ACTAGCCAACTACAGACAACACACTTTTAAACCAAAATTAGACTAATATAGTTGTCTCAACAGTG	28440
Db	28381	ACTAGCCAACTACAGACAACACACTTTTAAACCAAAATTAGACTAATATAGTTGTCTCAACAGTG	28440
Qy	28441	GAATCAAGTTTGCCATCTTCCATGCGCTTTGCTCACACCATTACCTTTTCTGGAATGTC	28500
Db	28441	GAATCAAGTTTGCCATCTTCCATGCGCTTTGCTCACACCATTACCTTTTCTGGAATGTC	28500
Qy	28501	CTGTACTCATCTCTCTGCTGTGAACCTCTATACCCAACTTTAAAAACCTAGCTCAAAAGTTC	28560
Db	28501	CTGTACTCATCTCTCTGCTGTGAACCTCTATACCCAACTTTAAAAACCTAGCTCAAAAGTTC	28560
Qy	28561	AACACTTCCATTCATTTCAAAAAGAGCTTCTCTCTCTTAAAGTTTAAAGATTAAGAACTCATTT	28620
Db	28561	AACACTTCCATTCATTTCAAAAAGAGCTTCTCTCTCTTAAAGTTTAAAGATTAAGAACTCATTT	28620
Qy	28621	TCATGAATCTTTTGGCAATTTATGCAACATGCTTGTGTTGCTGTTATTTGTGTTAGCC	28680
Db	28621	TCATGAATCTTTTGGCAATTTATGCAACATGCTTGTGTTGCTGTTATTTGTGTTAGCC	28680
Qy	28681	TCATATGCCCCCAAGTGTTTATAGACTCTCTTAAACGGCAAAAATGATGCTCTAAACACCTT	28740
Db	28681	TCATATGCCCCCAAGTGTTTATAGACTCTCTTAAACGGCAAAAATGATGCTCTAAACACCTT	28740
Qy	28741	TCATCTTTTCATAGTCTCTAGCTGTTGTTGCTATAAAGAAATACCTGAGGCTGGG	28800
Db	28741	TCATCTTTTCATAGTCTCTAGCTGTTGTTGCTATAAAGAAATACCTGAGGCTGGG	28800
Qy	28801	GAATTTTATTTAAAAAAGAGTTTATTTGGCTCACAGTTCTCGACTATATAAGAGCATA	28860
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Qy	28861	GTCTGACGATCTGCTTCAGTTCAGGCTTCAGGAAGTTTCCACCCTAGGTAGAGGCCAA	28920
Db	28861	GTCTGACGATCTGCTTCAGTTCAGGCTTCAGGAAGTTTCCACCCTAGGTAGAGGCCAA	28920
Qy	28921	GGGGACAGGCTATCATATCAAGAGAGAGAGAAAGAAAGAGAAAGAGAGGGTG	28980
Db	28921	GGGGACAGGCTATCATATCAAGAGAGAGAGAAAGAAAGAGAAAGAGAGGGTG	28980
Qy	28981	CATTCTTTTCAACATCAGTTCTTGTGGAGCTTATCGGACATATCGGACAGAGGCTGGCACGGTG	29040
Db	28981	CATTCTTTTCAACATCAGTTCTTGTGGAGCTTATCGGACATATCGGACAGAGGCTGGCACGGTG	29040
Qy	29041	GCTCATGCCCTGTAAATCCAGCCCTTTGGGAGACCAAGGTGGGTGGATCACCCTGAAGTCTAG	29100
Db	29041	GCTCATGCCCTGTAAATCCAGCCCTTTGGGAGACCAAGGTGGGTGGATCACCCTGAAGTCTAG	29100
Qy	29101	AAGCCTTGAGACGAGCTGGCCTGCTGTTGAGTAACTCCGCTCTCTACTTAAATAACAAAAT	29160
Db	29101	AAGCCTTGAGACGAGCTGGCCTGCTGTTGAGTAACTCCGCTCTCTACTTAAATAACAAAAT	29160
Qy	29161	TAGCTGGGCTGGTGGCGTGTAACCTAGTCCAGATACTCAGAGGCTCAGGTAGGATA	29220
Db	29161	TAGCTGGGCTGGTGGCGTGTAACCTAGTCCAGATACTCAGAGGCTCAGGTAGGATA	29220
Qy	29221	ATCATTGAAACCGGAGACAGAGGTTGAGTGGAGCTTGTGCCACTGCACTCCAGCGGG	29280
Db	29221	ATCATTGAAACCGGAGACAGAGGTTGAGTGGAGCTTGTGCCACTGCACTCCAGCGGG	29280
Qy	29281	GCAACAGAGTGAGCGGCTCAAAAAATTTTAAAAAATTTTAAATAATATAGACAGAGAA	29340
Db	29281	GCAACAGAGTGAGCGGCTCAAAAAATTTTAAAAAATTTTAAATAATATAGACAGAGAA	29340
Qy	29341	GCACCAAGTTATTCAGGAGGATCCACCCCAATGACTCAAAATACCTCCACAGGCGCTC	29400
Db	29341	GCACCAAGTTATTCAGGAGGATCCACCCCAATGACTCAAAATACCTCCACAGGCGCTC	29400

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Qy 32701 CTCTAGTATGACCTTCACTTTAAGGTACATGCAATGACTATTCCAGATAAGTTCACATTC 32760
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Db 32761 TGAAGAACTGGGAGTTAGGACTTCATATCTTTTGAAGGAACACAGTTTCAACCAATTAACAG 32820
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Qy	37081	TGTAATTAAGTGAAGTCTTCTAGAGAAAATGACAACTCAATTAATCTTAAATGTACCT	37140
Dd	37081	TGTAATTAAGTGAAGTCTTCTAGAGAAAATGACAACTCAATTAATCTTAAATGTACCT	37140
Qy	37141	CCAGAAAAAGCTGTCAAAGTGACATTTAGTAAATAGAGTACATTTCTCTAAGGCTTTG	37200
Dd	37141	CCAGAAAAAGCTGTCAAAGTGACATTTAGTAAATAGAGTACATTTCTCTAAGGCTTTG	37200
Qy	37201	CTTCTCCTCTGATTTCTATCATCTTTGAAGGTTATGTCATGGCTGACTTCAAAATCAAC	37260
Dd	37201	CTTCTCCTCTGATTTCTATCATCTTTGAAGGTTATGTCATGGCTGACTTCAAAATCAAC	37260
Qy	37261	TTTTAAATATTTATGGCCTTTCTTAAATGTAGTCTGAAGGTGAGGGCTTTATCTTT	37320
Dd	37261	TTTTAAATATTTATGGCCTTTCTTAAATGTAGTCTGAAGGTGAGGGCTTTATCTTT	37320
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Dd	37321	CTTTTGCTCCAGATTTTATACCGCTCATTTACCAAGCATCTTAAACAAAAACCTTAAA	37380
Qy	37381	ACAAAATCTTCTTGACCTGGTTTTCCACCTAGCTTAACATCTATTTTATCTTCCC	37440
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Dd	37441	CTTTGCACTAAAGCTTTTAAACGATCTTTATACCTCTGTCTCCATTTTCTCATCTGC	37500
Qy	37501	TAACTTATATGGCAAGATTAACCACTGCCTTTCAACATAATTTGGCCAACTCTACAGAACT	37560
Dd	37501	TAACTTATATGGCAAGATTAACCACTGCCTTTCAACATAATTTGGCCAACTCTACAGAACT	37560
Qy	37561	TTTCAAGTCTCTTTTAAATGACCACTCTGCTTACCTCCCTGCTTGTGACATCTTGC	37620
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Qy	37621	TTCTCACTTGGCACTTACCAAGTCTCAAGATTCCTCTCTTTAGGATGCTTTCAGAGCA	37680
Dd	37621	TTCTCACTTGGCACTTACCAAGTCTCAAGATTCCTCTCTTTAGGATGCTTTCAGAGCA	37680
Qy	37681	GCTACACAGTTGGTACTAATTAATTTATACATCCCTTTGACACAGGCTTGTGGGATTTGA	37740
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Qy	37741	TGGAGAGAGGAGAACTGGAGTGTAGTTCAGCCAGAGCTAGGGAATTTGCCATCTC	37800
Dd	37741	TGGAGAGAGGAGAACTGGAGTGTAGTTCAGCCAGAGCTAGGGAATTTGCCATCTC	37800
Qy	37801	CAGGTCTCAGGTCTGCAAGGGAGCTCACAGCTTTAACACATGGAGTCTAGAACTTTGTC	37860
Dd	37801	CAGGTCTCAGGTCTGCAAGGGAGCTCACAGCTTTAACACATGGAGTCTAGAACTTTGTC	37860
Qy	37861	TGGACCTTGACCAACACCGCCATGGATCCAAATACAGTGTCTCAATAGGATTTCCAGG	37920
Dd	37861	TGGACCTTGACCAACACCGCCATGGATCCAAATACAGTGTCTCAATAGGATTTCCAGG	37920
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Dd	37921	AAATTCGTATTTATTTAAAGAGAACTTACCAAGTGTGAGTCTGCTGTGGGCTTTGTG	37980
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Dd	38041	AATAGAGACAGAAAGGTAAACAGGTAAAGTGCAGAAATACATCAATTCAGCAATAGTG	38100
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Qy	38581	TAAACAACTTATAGACACATTTTAAAGTTTAAAGATCTCAAGAGCTATGCTGAATAGATA	38640
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Qy	38641	GGGTAAACAACTCTATTAAGTAAATAGGAAATTAACAGAAACAGTGAATTTCTTAATGAA	38700
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RESULT 2
AF222855 80622 bp DNA linear PRI 17-JUL-2000
LOCUS Homo sapiens clone HC chromosome 10 map 10q25.2 genomic sequence.
DEFINITION AF222855
ACCESSION AF222855
VERSION AF222855.1 GI:9246845
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 80622)
Barry.A.E., Bateman,M., Howman,E.V., Cancilla,M.R., Tainton,K.M.,
Irvine,D.V., Saffery,R. and Choo,K.H.
The 10q25 neocentromere and its inactive prosenitor have identical
primary nucleotide sequence: further evidence for epigenetic
modification
Genome Res. 10 (6), 832-838 (2000)
JOURNAL MEDLINE 20314874
PUBMED 10854414
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REFERENCE 2 (bases 1 to 80622)
AUTHORS Barry.A.E.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2000) Chromosome Research Unit, The Murdoch
Institute, 10th Floor, Royal Childrens Hospital, Flemington Rd.,
Parkville,, Melbourne, Victoria 3052, Australia
REMARK Genomic sequence from human 10q25.2, clone1b=HC
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7741 TTCAATTTAATGGGAACTCAAGAGTGTACATATAAGGAGGAACTGACAGTATGCTACAA 7800 Qy
7741 TTCAATTTAATGGGAACTCAAGAGTGTACATATAAGGAGGAACTGACAGTATGCTACAA 7800 Db
7801 GATAATACATCATATCAGTGAATGATATTCGCAAAAAGTCTATTTGATAGAGAAATAAT 7860 Qy
7801 GATAATACATCATATCAGTGAATGATATTCGCAAAAAGTCTATTTGATAGAGAAATAAT 7860 Db

Db	10021	GAATTAATATGTATAGCTCAGCTAAGCAAGATGAAGAGACCGCTAAATGTATACAA	10080
Qy	10081	ATATCTGAAACGTGCAAACTTTAAAGAGAGAGATTAAATTTTAACTGATACACGGGG	10140
Db	10081	ATATCTGAAACGTGCAAACTTTAAAGAGAGAGATTAAATTTTAACTGATACACGGGG	10140
Qy	10141	CACAATATGCAGTCCAGAGATGAATAATTTTACGCTGAGTATCTAGAAGAAATCCCCGATAG	10200
Db	10141	CACAATATGCAGTCCAGAGATGAATAATTTTACGCTGAGTATCTAGAAGAAATCCCCGATAG	10200
Qy	10201	TGAATCTGTTTAAAGGCTGCTGTAGTGTGGCCCTTTCCCTGGAGAGCAATAGAAATTTCAA	10260
Db	10201	TGAATCTGTTTAAAGGCTGCTGTAGTGTGGCCCTTTCCCTGGAGAGCAATAGAAATTTCAA	10260
Qy	10261	GTCTTACGATTTTAAAGTTTCTTGGGAACTAGATTTAGATTTAGATTTAGAGAAATTTATA	10320
Db	10261	GTCTTACGATTTTAAAGTTTCTTGGGAACTAGATTTAGATTTAGATTTAGAGAAATTTATA	10320
Qy	10321	TTAAATTTGGTCAGGTATGATAATGTGATTGTAGTTTCTATAAGAAAATTTGTATTTTTTAG	10380
Db	10321	TTAAATTTGGTCAGGTATGATAATGTGATTGTAGTTTCTATAAGAAAATTTGTATTTTTTAG	10380
Qy	10381	AGTTTACATACCTTGAATATATAAGCATAGAATATGATGTAGGAGATTGCTTTTAAATPACC	10440
Db	10381	AGTTTACATACCTTGAATATATAAGCATAGAATATGATGTAGGAGATTGCTTTTAAATPACC	10440
Qy	10441	ACAGTAGGAAGAAAGGAGGAGNAGAAAGAAAGGAAGGGAAGAAAGGGGAAAAAGA	10500
Db	10441	ACAGTAGGAAGAAAGGAGGAGNAGAAAGAAAGGAAGGGAAGAAAGGGGAAAAAGA	10500
Qy	10501	GGCAAGACGAAGAGAAAGGTAAAGACAAAGAAAAGAAATGAAGGAAGAGCTCGGCACCT	10560
Db	10501	GGCAAGACGAAGAGAGAGGTAAAGACAAAGAAAAGAAATGAAGGAAGAGCTCGGCACCT	10560
Qy	10561	GTGGCTCATGCTTATTAATCCAGCATTTAGGAGGCCAAGTTGGGAGGATCACTTTAATATA	10620
Db	10561	GTGGCTCATGCTTATTAATCCAGCATTTAGGAGGCCAAGTTGGGAGGATCACTTTAATATA	10620
Qy	10621	GCCCAGAGATTCAAGGCTGCAGTGAGCTGTGATTGGCCACTGCACTCCAGCCTCGGCTGG	10680
Db	10621	GCCCAGAGATTCAAGGCTGCAGTGAGCTGTGATTGGCCACTGCACTCCAGCCTCGGCTGG	10680
Qy	10681	CAGAGTCAAGCCCTGCTCTTAAAAAATAAATAAGTTTAAAAAGAAAGAAAGATAGAT	10740
Db	10681	CAGAGTCAAGCCCTGCTCTTAAAAAATAAATAAGTTTAAAAAGAAAGAAAGATAGAT	10740
Qy	10741	GAAGTAGGCAAGATGTGGTATGTTGAACCTGAAGGAAGTTAATATGTGAGTTCACCTT	10800
Db	10741	GAAGTAGGCAAGATGTGGTATGTTGAACCTGAAGGAAGTTAATATGTGAGTTCACCTT	10800
Qy	10801	TCCTCTTTCAGTCTTCTTTATGTATGTTTCCCACTTTCATAATAACAAATTTAAATATA	10860
Db	10801	TCCTCTTTCAGTCTTCTTTATGTATGTTTCCCACTTTCATAATAACAAATTTAAATATA	10860
Qy	10861	TTTTTCTGTCAAAACTTTAGTACAGTATTAATCCCTGGCTTCCTGACTAGAACAGCCT	10920
Db	10861	TTTTTCTGTCAAAACTTTAGTACAGTATTAATCCCTGGCTTCCTGACTAGAACAGCCT	10920
Qy	10921	CATTACACATGCGCAGAGTTTCTGGCCGACGAGGACACGCTAGTGGTTACCATTCTTGC	10980
Db	10921	CATTACACATGCGCAGAGTTTCTGGCCGACGAGGACACGCTAGTGGTTACCATTCTTGC	10980
Qy	10981	TCTGGTAAATGTGGTCTGGGCTGAAGGGCCCTTTCTAAGCTTCTAGATAGAAATCCAGGAA	11040
Db	10981	TCTGGTAAATGTGGTCTGGGCTGAAGGGCCCTTTCTAAGCTTCTAGATAGAAATCCAGGAA	11040
Qy	11041	ACTTGTTTAGAACTGCACACCTATCAGGCTACCTGTCAGGAGGTCAGTCTACTAAGGTGAAA	11100
Db	11041	ACTTGTTTAGAACTGCACACCTATCAGGCTACCTGTCAGGAGGTCAGTCTACTAAGGTGAAA	11100
Qy	11101	AAGCAGAGGGCAGAGGTCGTGATTAGCAGCTGACCCGCCCTGCTTTCTTCTGTCCTCATNT	11160
Db	11101	AAGCAGAGGGCAGAGGTCGTGATTAGCAGCTGACCCGCCCTGCTTTCTTCTGTCCTCATNT	11160

11161	QY	CGTGGAAATTCAGTGGAGCTCAAAATTTTGGTGGAGCTCTAAGTAGCTCCACTTGTAGAC	11222
11161	DB	CGTGGAAATTCAGTGGAGCTCAAAATTTTGGTGGAGCTCTAAGTAGCTCCACTTGTAGAC	11220
11221	QY	ATTGAGTGGAGCTCTAAGTGTCTTCAGAAATAGCAAAAACCTAGTATTTCTTTTCTTTTCT	11280
11221	DB	ATTGAGTGGAGCTCTAAGTGTCTTCAGAAATAGCAAAAACCTAGTATTTCTTTTCTTTTCT	11280
11281	QY	TTTTTTTTTTTTTTGGAGACAGAGCTTGGTCTGCGCCAGGCTGGAGTGCATATGGCAC	11340
11281	DB	TTTTTTTTTTTTTTGGAGACAGAGCTTGGTCTGCGCCAGGCTGGAGTGCATATGGCAC	11340
11341	QY	GATCTCCGCTCACTGAACCTCTGCCTCCCGGGTTAAGCGACTCTCTGCGCTCAGCTCCC	11400
11341	DB	GATCTCCGCTCACTGAACCTCTGCCTCCCGGGTTAAGCGACTCTCTGCGCTCAGCTCCC	11400
11401	QY	GAGTAGCTGGATTACAGTGGCCACACACGCCAGCTAATTTTCTATTTTAGTAG	11460
11401	DB	GAGTAGCTGGATTACAGTGGCCACACACGCCAGCTAATTTTCTATTTTAGTAG	11460
11461	QY	AGATGAGGTTTACCGTGTGGCAGCGTGTCTCAAACTCTGCGCTCAAGTATCGG	11520
11461	DB	AGATGAGGTTTACCGTGTGGCAGCGTGTCTCAAACTCTGCGCTCAAGTATCGG	11520
11521	QY	CTGCGTTGGCTCCCAAAGTCTCTGGGATTACAGTGTGAGCCACACACCCAGCTGCAAA	11580
11521	DB	CTGCGTTGGCTCCCAAAGTCTCTGGGATTACAGTGTGAGCCACACACCCAGCTGCAAA	11580
11581	QY	ACCTATTTTCTTGAATGGAGAAACATTTCCAAATCCAGAAAAATCGATAAAGCAGCA	11640
11581	DB	ACCTATTTTCTTGAATGGAGAAACATTTCCAAATCCAGAAAAATCGATAAAGCAGCA	11640
11641	QY	AAGAGGGTAAATTCATTAGTGAATAATTTCCAAATCCAGAAAAATCGATAAAGCAGCA	11700
11641	DB	AAGAGGGTAAATTCATTAGTGAATAATTTCCAAATCCAGAAAAATCGATAAAGCAGCA	11700
11701	QY	GCTTAAATTTTTTAAAGAAAGATTTTTTAAACTATCTCTTTGAGCCCTCTTTAGGAGA	11760
11701	DB	GCTTAAATTTTTTAAAGAAAGATTTTTTAAACTATCTCTTTGAGCCCTCTTTAGGAGA	11760
11761	QY	CCTCAGCTCTTGCCTTGAATGTGTAGAGTGGGAAATCCAGGGAGTTTGGAAATCATGTC	11820
11761	DB	CCTCAGCTCTTGCCTTGAATGTGTAGAGTGGGAAATCCAGGGAGTTTGGAAATCATGTC	11820
11821	QY	CTTATGCTGCTTTTGTGTGTAGAGAAATATAAATATTTATCTAGGTTTCTGCTGAT	11880
11821	DB	CTTATGCTGCTTTTGTGTGTAGAGAAATATAAATATTTATCTAGGTTTCTGCTGAT	11880
11881	QY	GGCAGTCAAGCATGAACACAAACCCTGTTGAGAAGCTGTAATTTCTGAATTTCTGCAG	11940
11881	DB	GGCAGTCAAGCATGAACACAAACCCTGTTGAGAAGCTGTAATTTCTGAATTTCTGCAG	11940
11941	QY	AGTGCACATCTAGGCCAGAAATTCGACATGAAGTGCAGTGGATTTAGCTCAGTGTAGG	12000
11941	DB	AGTGCACATCTAGGCCAGAAATTCGACATGAAGTGCAGTGGATTTAGCTCAGTGTAGG	12000
12001	QY	ATGAACCTCCAGAACCATTCGCTCTGACTGAAAGTGAAGCGGAGCGCGCTTGTGGAAAG	12060
12001	DB	ATGAACCTCCAGAACCATTCGCTCTGACTGAAAGTGAAGCGGAGCGCGCTTGTGGAAAG	12060
12061	QY	CTGCGTGAAGTCTCTCTCAATGAAGCGCATTTCTTTTCTCAGCCCGTCACTGTGTGGT	12120
12061	DB	CTGCGTGAAGTCTCTCTCAATGAAGCGCATTTCTTTTCTCAGCCCGTCACTGTGTGGT	12120
12121	QY	TTGGSCCCACGGTAAGCTCTCTGCGCTCTAGGCTGTAAACCCCAACCATCCTCTCTGCT	12180
12121	DB	TTGGSCCCACGGTAAGCTCTCTGCGCTCTAGGCTGTAAACCCCAACCATCCTCTCTGCT	12180
12181	QY	GGCTTCCAGAGTATTTGTTCTGAAGCAACAATCGATGTCAATCCCTTCTCTGAATCTCTA	12240
12181	DB	GGCTTCCAGAGTATTTGTTCTGAAGCAACAATCGATGTCAATCCCTTCTCTGAATCTCTA	12240

QY	12241	GCACCTACAGGAGCTCCATCCCTTGTGCCCCACATACCTCACACGTAGACATTCCTAATG	12300	Db	13321	TTTCGATCAATTCGTAATAATGTACAGATCCCAATCTGTCTCTGCATACATTTGCAATTT	13380
Db	12241	GCACCTACAGGAGCTCCATCCCTTGTGCCCCACATACCTCACACGTAGACATTCCTAATG	12300	QY	13381	ATAAAGCAGAGCAGACTAGCAGTCTTCTAATGCAATCCCCCAATGATGATGATGATTT	13440
QY	12301	AAGATTGATTGAATTAATGTAACCTCAGTGCTCCCACTCTCTAGTTGCCCTCTGCGC	12360	Db	13381	ATAAAGCAGAGCAGACTAGCAGTCTTCTAATGCAATCCCCCAATGATGATGATTT	13440
Db	12301	AAGATTGATTGAATTAATGTAACCTCAGTGCTCCCACTCTCTAGTTGCCCTCTGCGC	12360	QY	13441	AGATTGCTTCTCCCTATTTGGTTTCATGCAATGCTAAAGCTTTAAAGGATCATTCATTTTA	13500
QY	12361	TGCTTTGTACATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA	12420	Db	13441	AGATTGCTTCTCCCTATTTGGTTTCATGCAATGCTAAAGCTTTAAAGGATCATTCATTTTA	13500
Db	12361	TGCTTTGTACATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA	12420	QY	13501	ATTATTTAAATGTGTACAGCAGCTGAGCTTCCTTTCTTTTAAAGGAGAACCTTCAGG	13560
QY	12421	TGTTATCACCCAGCTCGAGTTTGTAGTGGCCCAATCTCAGCTCATCTGCAATTTACCTCCAG	12480	Db	13501	ATTATTTAAATGTGTACAGCAGCTGAGCTTCCTTTCTTTTAAAGGAGAACCTTCAGG	13560
Db	12421	TGTTATCACCCAGCTCGAGTTTGTAGTGGCCCAATCTCAGCTCATCTGCAATTTACCTCCAG	12480	QY	13561	GGCAATGCTTTAGTTTAAATGTTAAATCTCATTTTCTTTGAAAATAAGAACTTAAAG	13620
QY	12481	ATCAAGCAATCTCCACACTCAGCTCCCGAGAGCTGGACCATAGGACACCTGCCATAT	12540	Db	13561	GGCAATGCTTTAGTTTAAATGTTAAATCTCATTTTCTTTGAAAATAAGAACTTAAAG	13620
Db	12481	ATCAAGCAATCTCCACACTCAGCTCCCGAGAGCTGGACCATAGGACACCTGCCATAT	12540	QY	13621	CTGTATTACACAAAGCTCTCAAAGTGCAGATTTTCATTTGTTTAAACCATCTAGGA	13680
QY	12541	GCCCGGTAAATTTAATTTTGTAGAGATGGGGTTTCATCGTTTGCACAGCTAG	12600	Db	13621	CTGTATTACACAAAGCTCTCAAAGTGCAGATTTTCATTTGTTTAAACCATCTAGGA	13680
Db	12541	GCCCGGTAAATTTAATTTTGTAGAGATGGGGTTTCATCGTTTGCACAGCTAG	12600	QY	13681	AATGTTTGAATCTAATGAACATTAATGCTGAAATTTGGGCTGAAATTTCTGGGCTGAA	13740
QY	12601	TCTTGAACCTCTGAGCTCAGGCAATTCGCCGCTCTCAGTCTCCCAAGTGTGGGATTA	12660	Db	13681	AATGTTTGAATCTAATGAACATTAATGCTGAAATTTGGGCTGAAATTTCTGGGCTGAA	13740
Db	12601	TCTTGAACCTCTGAGCTCAGGCAATTCGCCGCTCTCAGTCTCCCAAGTGTGGGATTA	12660	QY	13741	ATATTGTTATAAATCTCAGTCTCAGTGTGTATTTATTTATTTCTTTCTTTCTTTT	13800
QY	12661	AGCGGTGAGCCACCATGCCAGCGCTAGCACTCATCTTAAATGCTATATTTACTTATCTG	12720	Db	13741	ATATTGTTATAAATCTCAGTCTCAGTGTGTATTTATTTATTTCTTTCTTTCTTTT	13800
Db	12661	AGCGGTGAGCCACCATGCCAGCGCTAGCACTCATCTTAAATGCTATATTTACTTATCTG	12720	QY	13801	TGACCCGATATAGATGAAGCAGAGCAAGGAGCAATCCCATGTGAATAGAAAGGCG	13860
QY	12721	GCTTTCCCAACAGCTGCGGGCTCTTCAAGAGTAAATGCAATGTTTTCACCTTTATTTCC	12780	Db	13801	TGACCCGATATAGATGAAGCAGAGCAAGGAGCAATCCCATGTGAATAGAAAGGCG	13860
Db	12721	GCTTTCCCAACAGCTGCGGGCTCTTCAAGAGTAAATGCAATGTTTTCACCTTTATTTCC	12780	QY	13861	AGCCTGAAATGCTGCTGCTTTTGAATTTAAAGCTGGTTTTCGATTTAAATTCAGTAAA	13920
QY	12781	CCAGTTTGTGGCACTTAGGCACTCGGCATCAATGAATTAACCTCTGAGCTGTGATA	12840	Db	13861	AGCCTGAAATGCTGCTGCTTTTGAATTTAAAGCTGGTTTTCGATTTAAATTCAGTAAA	13920
Db	12781	CCAGTTTGTGGCACTTAGGCACTCGGCATCAATGAATTAACCTCTGAGCTGTGATA	12840	QY	13921	TGGTCCAGGACTATAAATGTTGAACATTTTTCACCTGTGATTTTAAATTTTAGTCTTAT	13980
QY	12841	TTACAAACGTGGAAGATGACGAGCACTCAGCAACTTTTCAGTGAGTAAACAAAGGCTTTC	12900	Db	13921	TGGTCCAGGACTATAAATGTTGAACATTTTTCACCTGTGATTTTAAATTTTAGTCTTAT	13980
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QY	12901	ATTTCAGATGATTTATGACTGCGCAATCTGGGCTGCTTCTGCTGTGGTTCAAGGAG	12960	Db	13981	GTTTATTTTATTTTGTGATGTTTACATTTTCCCATGGGAGCAGCTATGTCATGTCGGC	14040
Db	12901	ATTTCAGATGATTTATGACTGCGCAATCTGGGCTGCTTCTGCTGTGGTTCAAGGAG	12960	QY	14041	ATGATTTCATCATGTAAATCTCGGGTATTTTGGTTTGTGTTATGTTTCAAGAAAGCGGAA	14100
QY	12961	AGCATAGTCTACAGAACCCAGAGACCTGGGTACTCTGGAAGTTAGACTTAAGCCCAACCCG	13020	Db	14041	ATGATTTCATCATGTAAATCTCGGGTATTTTGGTTTGTGTTATGTTTCAAGAAAGCGGAA	14100
Db	12961	AGCATAGTCTACAGAACCCAGAGACCTGGGTACTCTGGAAGTTAGACTTAAGCCCAACCCG	13020	QY	14101	TGCCAAAATAAAGAGGTTTGTGATGCTAGTGTCTCTTCCCTTAAACAAATCAAGGCG	14160
QY	13021	GTCCCTTGAATGGGAAATATTTCCCTTCAATCTCTGTTTGTAGGACAGAAAGATGAGTA	13080	Db	14101	TGCCAAAATAAAGAGGTTTGTGATGCTAGTGTCTCTTCCCTTAAACAAATCAAGGCG	14160
Db	13021	GTCCCTTGAATGGGAAATATTTCCCTTCAATCTCTGTTTGTAGGACAGAAAGATGAGTA	13080	QY	14161	TTTTATTTAAATCCACTTAATGGGACACTGCGAGAAATTTAAATAATGGAAGTCCCATCCAC	14220
QY	13081	ATCCAGTGATACATGCTGGAATGTTTATTTCCACTACCGAGCTGCTCTCAACTTAAC	13140	Db	14161	TTTTATTTAAATCCACTTAATGGGACACTGCGAGAAATTTAAATAATGGAAGTCCCATCCAC	14220
Db	13081	ATCCAGTGATACATGCTGGAATGTTTATTTCCACTACCGAGCTGCTCTCAACTTAAC	13140	QY	14221	AGAGGCGAGGTACTATGATGTAAGATTTAGTTAGTTGGGGATTAATAGATGATCATATAA	14280
QY	13141	AATCCATGAAAGAAACAAGATGATATATACTTTTCTAATTTGTGATGCCCTTTGTTTAT	13200	Db	14221	AGAGGCGAGGTACTATGATGTAAGATTTAGTTAGTTGGGGATTAATAGATGATCATATAA	14280
Db	13141	AATCCATGAAAGAAACAAGATGATATATACTTTTCTAATTTGTGATGCCCTTTGTTTAT	13200	QY	14281	TTTTATGAGCTAAACCGGAGGCACTTTTCTTTTTCAGATCGAGTCTCACTGTGCTTAGGC	14340
QY	13201	TTGTTTCCGTTTAAAGAGGAGGTGCAATGTAATTTGTTTGGTTTGGTTTCTCTTCTTC	13260	Db	14281	TTTTATGAGCTAAACCGGAGGCACTTTTCTTTTTCAGATCGAGTCTCACTGTGCTTAGGC	14340
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QY	13261	AATAAGAGCATCTTAATATAAAGTACAGTGCACATCTGCCATTTTCAAAAATTAACAAG	13320	Db	14341	TGGAGTGCAGTGCAGTGCATCAGCTCACTCCGCTCCCGCTCCCGGTTTCAAGCGGAT	14400
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Qy 16414 CAGTCCCAAGCAAAACCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16473
Db 16441 CAGTCCCAAGCAAAACCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16500
Qy 16474 CATGAGTCTATTCTCCGCAAACTGCGATAGGTAAAGTAGAGACTGCGGAAGAGCAAGTTT 16533
Db 16501 CATGAGTCTATTCTCCGCAAACTGCGATAGGTAAAGTAGAGACTGCGGAAGAGCAAGTTT 16560
Qy 16534 GCAAGTCCAGAGAAATGAAAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16593
Db 16561 GCAAGTCCAGAGAAATGAAAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16620

QY	16594	TATCCGATGGATGGCCCTTAAAGTGAGCTCAAGGCTTAAGGGAGAGATAGGGGCTGATGA	16653	Db	17701	TGGAGGTTGTAGTAAGCAAGATTGGCCACTCATGCCAGCTGGCGACAGAGCAAGA	17760
Db	16621	TATCCGATGGATGGCCCTTAAAGTGAGCTCAAGGCTTAAGGGAGAGATAGGGGCTGATGA	16680	QY	17734	CTTTCTTAAACACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC	17793
QY	16654	TCTGAGATTTCATCAGTGTGTGGCTGATGTTTAAACCCAGGGGACAGAGATGAAGGTTAT	16713	Db	17761	CTTTCTTAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	17820
Db	16681	TCTGAGATTTCATCAGTGTGTGGCTGATGTTTAAACCCAGGGGACAGAGATGAAGGTTAT	16740	QY	17794	AAAGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA	17853
QY	16714	TCCAGGGAGAGCGTAGATAAAGAGCTAAATGGCTTCTGGTCCCTTAGTCATTCAAAATC	16773	Db	17821	AAAGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA	17880
Db	16741	TCCAGGGAGAGCGTAGATAAAGAGCTAAATGGCTTCTGGTCCCTTAGTCATTCAAAATC	16800	QY	17854	ARGGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAAA	17913
QY	16774	GGACCTCTGAGGACAGAGAGAAACCCAGAAAGATAGATTCCTGGGACTCAGGGATAAA	16833	Db	17881	ARGGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAAA	17940
Db	16801	GGACCTCTGAGGACAGAGAGAAACCCAGAAAGATAGATTCCTGGGACTCAGGGATAAA	16860	QY	17914	GAATAATACCTCCAGAGAGCCAGGCTCTCTTAGGCCTCTCTGAGAACTCACATCCCTTTGA	17973
QY	16834	GACTTTCAAAAAGTGGGGCTGGCCAGTGTCTGGAAGAACTAGCAGGACCGGACACAGA	16893	Db	17941	GAATAATACCTCCAGAGAGCCAGGCTCTCTTAGGCCTCTCTGAGAACTCACATCCCTTTGA	18000
Db	16861	GACTTTCAAAAAGTGGGGCTGGCCAGTGTCTGGAAGAACTAGCAGGACCGGACACAGA	16920	QY	17974	TGAACACAATGCTTCACACTCTCAATGTTATTTGGTAACTCCAACTTATCAATATACCTAA	18033
QY	16894	AGGGTAATCGTTGGACCTCGAGAACTTGAATTTGAATTTAAAGTTTGGTAACTTTAAAAA	16953	Db	18001	TGAACACAATGCTTCACACTCTCAATGTTATTTGGTAACTCCAACTTATCAATATACCTAA	18060
Db	16921	AGGGTAATCGTTGGACCTCGAGAACTTGAATTTGAATTTAAAGTTTGGTAACTTTAAAAA	16980	QY	18034	ATCACTTAGTACTGAACTCTGGCATATAGTAACTCACCTAAATGAAGAGATAAGAGTCATGGA	18093
QY	16954	AGAGCAATTTAGATACCTTTGAAATTTATTTGCAAGATTTGTTGGTATATGTTATT	17013	Db	18061	ATCACTTAGTACTGAACTCTGGCATATAGTAACTCACCTAAATGAAGAGATAAGAGTCATGGA	18120
Db	16981	AGAGCAATTTAGATACCTTTGAAATTTATTTGCAAGATTTGTTGGTATATGTTATT	17040	QY	18094	GTATTTGAGCAATTAAGATTAAGTACCTCAATATATACATGTCACAAAGTTTGGATCT	18153
QY	17014	CCAGGCAAGGGACACAGAAAGTAAATAATCTTACTGAACAGTTTACTGCATGCGCTGGCA	17073	Db	18121	GTATTTGAGCAATTAAGATTAAGTACCTCAATATATACATGTCACAAAGTTTGGATCT	18180
Db	17041	CCAGGCAAGGGACACAGAAAGTAAATAATCTTACTGAACAGTTTACTGCATGCGCTGGCA	17100	QY	18154	TAAAAACCGACTCAGTGCAGTAAAGGAAAGGAAAGATACATAACACGGTACCATATGTA	18213
QY	17074	CTGTAAACACCTGTTTAAATCTCACGGCAACCTATAGATAGGTTGTCTATCCCTATC	17133	Db	18181	TAAAAACCGACTCAGTGCAGTAAAGGAAAGGAAAGATACATAACACGGTACCATATGTA	18240
Db	17101	CTGTAAACACCTGTTTAAATCTCACGGCAACCTATAGATAGGTTGTCTATCCCTATC	17160	QY	18214	AAATTGATAATATATGCTTACCAATTTGTAAAGACACATACAAATAGATACATGTATTT	18273
QY	17134	TTACAGATGAGGATATGAGGTGACGTAGATTAAGCAGTTTGCTCAGGTTCACCAACT	17193	Db	18241	AAATTGATAATATATGCTTACCAATTTGTAAAGACACATACAAATAGATACATGTATTT	18300
Db	17161	TTACAGATGAGGATATGAGGTGACGTAGATTAAGCAGTTTGCTCAGGTTCACCAACT	17220	QY	18274	AAATATACTCGAACGGTTTACCTATGGGTGCTGCTGGAGTGGGGTAAAGTCCGTAAGCT	18333
QY	17194	GGTTAAGCTAGAGCTAGGATTTGAAACCGGATGGGCTGATCCAGAGCTCATGCTTTAAA	17253	Db	18301	AAATATACTCGAACGGTTTACCTATGGGTGCTGCTGGAGTGGGGTAAAGTCCGTAAGCT	18360
Db	17221	GGTTAAGCTAGAGCTAGGATTTGAAACCGGATGGGCTGATCCAGAGCTCATGCTTTAAA	17280	QY	18334	GTATGGAAACCTTAAACAAATACATGAAACGAGTAGGAATCAGAAGGAGTAAACAATAAAA	18393
QY	17254	TCGCTAGACTGGTCTCAGAGAGA CTGGACCCGAAATAATTAATAAATAATTAAGA	17313	Db	18361	GTATGGAAACCTTAAACAAATACATGAAACGAGTAGGAATCAGAAGGAGTAAACAATAAAA	18420
Db	17281	TCGCTAGACTGGTCTCAGAGAGA CTGGACCCGAAATAATTAATAAATAATTAAGA	17340	QY	18394	TGTGCCATGAACCTGAGGAGTGTAAATTAATCAACTCAGTGCATCTGAGTTTAAATAAGA	18453
QY	17314	GCCCCCTGGCTAGCAAAATTAGGATTGTTTCAGACACAGATGTGAAAAGGAAAGCAAGCAG	17373	Db	18421	TGTGCCATGAACCTGAGGAGTGTAAATTAATCAACTCAGTGCATCTGAGTTTAAATAAGA	18480
Db	17341	GCCCCCTGGCTAGCAAAATTAGGATTGTTTCAGACACAGATGTGAAAAGGAAAGCAAGCAG	17400	QY	18454	AAGATGATAATTTGTTTATTTATTACTCGTAGGCTTCCACTTGCACTCAGCTTTTACAAT	18513
QY	17374	AGGAAAGTCACTGTACAGAAAGAGAGACCCATGACAGACAGACAGATGAGCTGTATA	17433	Db	18481	AAGATGATAATTTGTTTATTTATTACTCGTAGGCTTCCACTTGCACTCAGCTTTTACAAT	18540
Db	17401	AGGAAAGTCACTGTACAGAAAGAGAGACCCATGACAGACAGACAGATGAGCTGTATA	17460	QY	18514	GTGGAGTATCTTCCAGATGGCACCCCTTGGACTTGGCTCAGGAGGAGAGCTTTTTC	18573
QY	17434	GTGGCTGGCATCTAGCCCTGAAATPACCTCAGAGAGGACGGCTCAGCCCTGTAATCC	17493	Db	18541	GTGGAGTATCTTCCAGATGGCACCCCTTGGACTTGGCTCAGGAGGAGAGCTTTTTC	18600
Db	17461	GTGGCTGGCATCTAGCCCTGAAATPACCTCAGAGAGGACGGCTCAGCCCTGTAATCC	17520	QY	18574	TCCAGCTTTCTAGGTTGATTTAATATATCAGGGATTAAGTATAAATAAAGGACGCTGCTC	18633
QY	17494	CAGCACTTTGGAGGCGGAGTGGGACAGATCACTGTAGGTCAGGAGTTTGAGACCAAGCT	17553	Db	18601	TCCAGCTTTCTAGGTTGATTTAATATATCAGGGATTAAGTATAAATAAAGGACGCTGCTC	18660
Db	17521	CAGCACTTTGGAGGCGGAGTGGGACAGATCACTGTAGGTCAGGAGTTTGAGACCAAGCT	17580	QY	18634	CCTGGGTAGCCCTTCTGGACTTCAGAGCTAAATTTGCAAAAGTCAGTTTACATGTGATTT	18693
QY	17554	GGCCAAATGGGAAATCCCGTCTCTACTAAAAATACAAATTAAGCCAGCATGCTGACAG	17613	Db	18661	CCTGGGTAGCCCTTCTGGACTTCAGAGCTAAATTTGCAAAAGTCAGTTTACATGTGATTT	18720
Db	17581	GGCCAAATGGGAAATCCCGTCTCTACTAAAAATACAAATTAAGCCAGCATGCTGACAG	17640	QY	18694	TCATCTATGAATTAAGGCAAGGTAGAAAATGCGACAGAAAATATGATTTATTATGG	18753
QY	17614	GCACCTGTATCCAGCTGTTTCACTTGGCTGAGTCAGGAGAAATAGCTGGATCCGGGAAG	17673	Db	18721	TCATCTATGAATTAAGGCAAGGTAGAAAATGCGACAGAAAATATGATTTATTATGG	18780
Db	17641	GCACCTGTATCCAGCTGTTTCACTTGGCTGAGTCAGGAGAAATAGCTGGATCCGGGAAG	17700	QY	18754	TGTTACTATCCCTTACAAGCGGAGTGTGAGTGCCTCTTTTGTCCACTGATTTAAGCA	18813
QY	17674	TGGAGGTTGTAGTAAGCAAGATTGGCCACTGCATGCCAGCTGGCGACAGAGCAAGA	17733				

Db	18781	TGTTACTATCCCTTACAAAGCGAGTGTACAGTGGCTCTTTTGTGTCACCTGATTTAAGGCA	18840
Qy	18814	AGATGAACAGAAAGTGTCTATGATCAGCTCTTCAAAAGCACACTCTGGCCCTCGGCTGC	18873
Db	18841	AGATGAACAGAAAGTGTCTATGATCAGCTCTTCAAAAGCACACTCTGGCCCTCGGCTGC	18900
Qy	18874	AGGCGCCCTGCACATTCCTCCAGCTGCGTGTCCGCTGGTGACACAGTGCATAAATGTGGCG	18933
Db	18901	AGGCGCCCTGCACATTCCTCCAGCTGCGTGTCCGCTGGTGACACAGTGCATAAATGTGGCG	18960
Qy	18934	CTTCTCTGGTGCAAACTGTCTCACTTAGCTCCGCTCTTGTGGCACAGCAGCAAGAGGAA	18993
Db	18961	CTTCTCTGGTGCAAACTGTCTCACTTAGCTCCGCTCTTGTGGCACAGCAGCAAGAGGAA	19020
Qy	18994	ATCGAAATGTTGGATTTCAAGGTAAACAAGAGCTGGAAACAACACTACTGGCCGAGTC	19053
Db	19021	ATCGAAATGTTGGATTTCAAGGTAAACAAGAGCTGGAAACAACACTACTGGCCGAGTC	19080
Qy	19054	TGAGAGTTTCAGCGAGACTGGTGACGCTTGTGTTTTTCCACTGACAGCTGAAATATGAG	19113
Db	19081	TGAGAGTTTCAGCGAGACTGGTGACGCTTGTGTTTTTCCACTGACAGCTGAAATATGAG	19140
Qy	19114	CCAGCTTCAGTGAAGCTTCTTCCCTCCCTCCCTCAAGGTACCCACAATCTCAGTTCT	19173
Db	19141	CCAGCTTCAGTGAAGCTTCTTCCCTCCCTCCCTCAAGGTACCCACAATCTCAGTTCT	19200
Qy	19174	CTCAGGAAGCCAAAATAAGATTTGAGGGTTTAGGATTTGGTGTCTTTATCTATTACA	19233
Db	19201	CTCAGGAAGCCAAAATAAGATTTGAGGGTTTAGGATTTGGTGTCTTTATCTATTACA	19260
Qy	19234	GGATGTAAATATGTTCTCCACCAGATGTTCTGCTTGTAAACAATACTCACTTCCTGACA	19293
Db	19261	GGATGTAAATATGTTCTCCACCAGATGTTCTGCTTGTAAACAATACTCACTTCCTGACA	19320
Qy	19294	CTACTGCATATGAGAGGTGTTACTACCAAGGTAAACAGAAATGGCTGCCCAATTCGA	19353
Db	19321	CTACTGCATATGAGAGGTGTTACTACCAAGGTAAACAGAAATGGCTGCCCAATTCGA	19380
Qy	19354	AATCCCTGAACTGAGTGAGAGAAATCAGAAATATATATAGGGATTCACAGAGCTGGCTA	19413
Db	19381	AATCCCTGAACTGAGTGAGAGAAATCAGAAATATATATAGGGATTCACAGAGCTGGCTA	19440
Qy	19414	CGATGTGCCAGTGTGCAGATCTTGTCTCATCATCAGCAGGTGTGCTGTCTAGCAAC	19473
Db	19441	CGATGTGCCAGTGTGCAGATCTTGTCTCATCATCAGCAGGTGTGCTGTCTAGCAAC	19500
Qy	19474	TGCTCACTGCTTCAATTCCTGCTGCTGCTTGTAAATACCTGCTTTCTCAGCTCAATTTGC	19533
Db	19501	TGCTCACTGCTTCAATTCCTGCTGCTGCTTGTAAATACCTGCTTTCTCAGCTCAATTTGC	19560
Qy	19534	TTTCTTCCCTGTGGAGTCAAGCTTCTTGGGTCAACAGCAAAATGATTTTGAATCA	19593
Db	19561	TTTCTTCCCTGTGGAGTCAAGCTTCTTGGGTCAACAGCAAAATGATTTTGAATCA	19620
Qy	19594	CCGTGTACTCAAGAGAGCTACAGACATTTGGGCATCCCTCCACTCTCTTGGAAACA	19653
Db	19621	CCGTGTACTCAAGAGAGCTACAGACATTTGGGCATCCCTCCACTCTCTTGGAAACA	19680
Qy	19654	ATTTTATGAAGCAAGGTGGCATAGTGCCTCTTGGAGTGTGTTGCTCAGCCAGGCCCC	19713
Db	19681	ATTTTATGAAGCAAGGTGGCATAGTGCCTCTTGGAGTGTGTTGCTCAGCCAGGCCCC	19740
Qy	19714	AGCTTTGTCTCAACATGAAATTTAGAGAGCTTCAGAACAGATCCACATTTTCAATG	19773
Db	19741	AGCTTTGTCTCAACATGAAATTTAGAGAGCTTCAGAACAGATCCACATTTTCAATG	19800
Qy	19774	GCCTCACCAACTGGATAAAGAACAAATGGCCATATCTCAATGACCACTTTTTCAGGTG	19833
Db	19801	GCCTCACCAACTGGATAAAGAACAAATGGCCATATCTCAATGACCACTTTTTCAGGTG	19860
Qy	19834	GGATGTAGATGCTGGAATTTGGGTACAGCAATTTGCCCAACCAAACTTTGCAAAAAGGCTG	19893
Db	19861	GGATGTAGATGCTGGAATTTGGGTACAGCAATTTGCCCAACCAAACTTTGCAAAAAGGCTG	19920
Qy	19894	GAAGCTCTGACTGGGAGCCCTAAATATGCAAAAGTTTGATAGGCTCTTTCATGCAGAAATG	19953
Db	19921	GAAGCTCTGACTGGGAGCCCTAAATATGCAAAAGTTTGATAGGCTCTTTCATGCAGAAATG	19980
Qy	19954	AACCCCGTGTATGATATAGTAAAGGGTTGGCCCTTTATGTTTCTATCTCTTACAAACC	20013
Db	19981	AACCCCGTGTATGATATAGTAAAGGGTTGGCCCTTTATGTTTCTATCTCTTACAAACC	20040
Qy	20014	TGGTAGAATAGATATGTTTTCCTTTTAAAAAATGTCAACAATTCATTTATGATGCT	20073
Db	20041	TGGTAGAATAGATATGTTTTCCTTTTAAAAAATGTCAACAATTCATTTATGATGCT	20100
Qy	20074	GTGTATAGTAATCACTCAGATCATGCTCCATGAAAATGCTTCAGAACCAATATAAGGAGA	20133
Db	20101	GTGTATAGTAATCACTCAGATCATGCTCCATGAAAATGCTTCAGAACCAATATAAGGAGA	20160
Qy	20134	TTTTTTAGCCATGTGTGACAAAGAGAGGCCATTTTCAAGTGTGAAAATTTGTTTCAAGAGT	20193
Db	20161	TTTTTTAGCCATGTGTGACAAAGAGAGGCCATTTTCAAGTGTGAAAATTTGTTTCAAGAGT	20220
Qy	20194	ATTTGATATGTTTTTCTCAGATCTTTTATTTTTTATTTTTTTTGAACAGAGTCTCACCT	20253
Db	20221	ATTTGATATGTTTTTCTCAGATCTTTTATTTTTTATTTTTTTTGAACAGAGTCTCACCT	20280
Qy	20254	TGTCACCCAGGCTGGAGTACAGTGGCTGTGGTCTCGCTCACCTGCAACCTCTGCCTCCCA	20313
Db	20281	TGTCACCCAGGCTGGAGTACAGTGGCTGTGGTCTCGCTCACCTGCAACCTCTGCCTCCCA	20340
Qy	20314	GGTTCAAGCGATTTCTCTGTGAGCTTCCCGAATAGCTGGGATTTACAGGGCATGCAACCAC	20373
Db	20341	GGTTCAAGCGATTTCTCTGTGAGCTTCCCGAATAGCTGGGATTTACAGGGCATGCAACCAC	20400
Qy	20374	CATGCCCTAAATTTTGTATTTTATAGTAGACAGAGTTTCCGCTGTTGACAGGCTTGC	20433
Db	20401	CATGCCCTAAATTTTGTATTTTATAGTAGACAGAGTTTCCGCTGTTGACAGGCTTGC	20460
Qy	20434	TTGAACCTCTGACTCAGGTGATCCACCCACCTCAGCTCCCAAGCAGCTGGGATTTACAG	20493
Db	20461	TTGAACCTCTGACTCAGGTGATCCACCCACCTCAGCTCCCAAGCAGCTGGGATTTACAG	20520
Qy	20494	GCATGACCAACCGTGGCCAGCTGTTTTCTCAGATCTCTGATTTTGTCTGAAAGCTTCA	20553
Db	20521	GCATGACCAACCGTGGCCAGCTGTTTTCTCAGATCTCTGATTTTGTCTGAAAGCTTCA	20580
Qy	20554	TTTCTATCTTCTTATTTTCAATTTTGGAAAGTAGTACACCTAAGTAAGTTTTTAAACAATA	20613
Db	20581	TTTCTATCTTCTTATTTTCAATTTTGGAAAGTAGTACACCTAAGTAAGTTTTTAAACAATA	20640
Qy	20614	TATCTTTGAAAAATTCCTGGTTTCTTTCTTATTTCTCAAAAAATATGTTCAAGTATGCT	20673
Db	20641	TATCTTTGAAAAATTCCTGGTTTCTTTCTTATTTCTCAAAAAATATGTTCAAGTATGCT	20700
Qy	20674	GATGTTATGTTTCTTCAAAATTTTCAATTTTCTATCTCAGATTTTATCTCATGCTTAAT	20733
Db	20701	GATGTTATGTTTCTTCAAAATTTTCAATTTTCTATCTCAGATTTTATCTCATGCTTAAT	20760
Qy	20734	TGTTATTTGAATAGTCTTCTCTTCTTCTCAGTTTCTTGGTCTCTTATTTTCACTCTAAG	20793
Db	20761	TGTTATTTGAATAGTCTTCTCTTCTTCTCAGTTTCTTGGTCTCTTATTTTCACTCTAAG	20820
Qy	20794	TCTAAGTGGCTATTAAGATAAGAGCTGTGAACAGATCTTCTTCTTCTTCTTCTTATCT	20853
Db	20821	TCTAAGTGGCTATTAAGATAAGAGCTGTGAACAGATCTTCTTCTTCTTCTTCTTATCT	20880
Qy	20854	TTTGACTGTGATGCGAGTGAACAACTGTTAACTGTTTTTGTATTTCTTCAATCACTTCCACAGA	20913
Db	20881	TTTGACTGTGATGCGAGTGAACAACTGTTAACTGTTTTTGTATTTCTTCAATCACTTCCACAGA	20940
Qy	20914	ACATGCTGACTCTCTCTCTGAAAGCAATGCCCAAGCAGCAATTTGTAGATGATG	20973
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Db	25381	TGCCATACCA	CAATTTAGTTC	TATATCTGCTTAGGCTCCCTCTTGGCTAGAGTATTTA	25440
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RP11-383C6 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACE3.6.

FEATURES

source

Location/Qualifiers

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ORIGIN

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Db 72093 GAATGCAATAAAGATGAAGTATGCTGTAAATATTTTCAAGCTTTCCAGCAATAGGTTT 72152
QY 3598 CTGTTGCAACTGCTCACTCTGCCATTTAGCAATGAAAGCAGCTATAGAAATATACATA 3657
Db 72153 CTGTTGCAACTGCTCACTCTGCCATTTAGCAATGAAAGCAGCTATAGAAATATACATA 72212
QY 3658 AATGAGCCTGTAAATCCCAACACTTTTGGAGCCCAAGTGGATGGATCACTTGAGGTCAG 3717
Db 72213 AATGAGCCTGTAAATCCCAACACTTTTGGAGCCCAAGTGGATGGATCACTTGAGGTCAG 72272
QY 3718 GAATTCGAGACCTTGGCCCAACATGCGCAAAACCCCGTCTCTACTAAAAATACAAAAAT 3777
Db 72273 GAATTCGAGACCTTGGCCCAACATGCGCAAAACCCCGTCTCTACTAAAAATACAAAAAT 72332
QY 3778 GAGCCAGGACTTACGATGCTGTAGTCCAGCTACTTGGAGGCTGAGGAGGAGATCT 3837
Db 72333 GAGCCAGGACTTACGATGCTGTAGTCCAGCTACTTGGAGGCTGAGGAGGAGATCT 72392
QY 3838 CTTGAAACCCGGGAAGGGAGGTTACAGTGAGCCAAAGATTGTGCCACTGCACTCCAGCCTG 3897
Db 72393 CTTGAAACCCGGGAAGGGAGGTTACAGTGAGCCAAAGATTGTGCCACTGCACTCCAGCCTG 72452
QY 3898 GGCAACAGAGTGAGACTGCTCTCAAAAAAATAAAGGAAAGAAATACACATAATG 3957
Db 72453 GGCAACAGAGTGAGACTGCTCTCAAAAAAATAAAGGAAAGAAATACACATAATG 72512
QY 3958 AATGATGTGGCTGTGACAGATATATCTCATGCTCTAGCTTGGCAACCCCTTGTCTTAC 4017
Db 72513 AATGATGTGGCTGTGACAGATATATCTCATGCTCTAGCTTGGCAACCCCTTGTCTTAC 72572
QY 4018 ACTGTCTAGTTTACCTCTTAAGAGATTAATAATCAACATATCTATTAGCTTTATTCAC 4077
Db 72573 ACTGTCTAGTTTACCTCTTAAGAGATTAATAATCAACATATCTATTAGCTTTATTCAC 72632
QY 4078 ATCCTAGTGTCAATTTCTTCTTATGAGAAATCAAAATTTCTGTTGATCATATTTCTTC 4137

Db 72633 ATCCTAGTGTCAATTTCTTCTATGTAGAAATCAAAATTTTCAATCTGGTATCATATTTCTTC 72692
Qy 4138 TTTCRAAATAATTTCCCTTTAAATATTTTATAGCAGGCTTAATAGCAATGCAATATGC 4197
Db 72693 TTTCRAAATAATTTCCCTTTAAATATTTTATAGCAGGCTTAATAGCAATGCAATATGC 72752
Qy 4198 AATTCATTCGTATAGACCTGTGCTATATAAATAGCAATGAATATGTGTCAGTTTTTATTTG 4257
Db 72753 AATTCATTCGTATAGACCTGTGCTATATAAATAGCAATGAATATGTGTCAGTTTTTATTTG 72812
Qy 4258 TCTGAAAAAGTTTTTTGTTTTGAAATATACATTTTGTGCGGTATATAAATCAAGTTGCA 4317
Db 72813 TCTGAAAAAGTTTTTTGTTTTGAAATATACATTTTGTGCGGTATATAAATCAAGTTGCA 72872
Qy 4318 TAACCTCTCTTTCTTTCAGCACCTTAAATGAAGTCACTCAAGTTATCTTCTGGCTTGTATAG 4377
Db 72873 TAACCTCTCTTTCTTTCAGCACCTTAAATGAAGTCACTCAAGTTATCTTCTGGCTTGTATAG 72932
Qy 4378 TTTCCTGCTGCTCCTTCAAGATTTTTCATTTGCTTTTAAATTTTATAGCAATTTGATGTCT 4437
Db 72933 TTTCCTGCTGCTCCTTCAAGATTTTTCATTTGCTTTTAAATTTTATAGCAATTTGATGTCT 72992
Qy 4438 TAGGAGTGAATTTCTTTGATATATCTTTTGGGGCTCTTAAATTTCTTTCATCTTTT 4497
Db 72993 TAGGAGTGAATTTCTTTGATATATCTTTTGGGGCTCTTAAATTTCTTTCATCTTTT 73052
Qy 4498 TTTCCTTTTTTTTTTTTTTAAATCAAGTTTGTCTGCTCTCCTCAAGTGGGCTGAAAAAAA 4557
Db 73053 TTTCCTTTTTTTTTTTTTTAAATCAAGTTTGTCTGCTCTCCTCAAGTGGGCTGAAAAAAA 73112
Qy 4558 AAGAAAAATAAATCATAGTTTAAATACTAATTTTGGAAAAATTTTTCAGCTATCATTTCT 4617
Db 73113 AAGAAAAATAAATCATAGTTTAAATACTAATTTTGGAAAAATTTTTCAGCTATCATTTCT 73172
Qy 4618 TCAAAATATTTATCCTACTCTATGCTCCCTCCCTCCCTCTCTCTCTGCTGACTCAAAATAC 4677
Db 73173 TCAAAATATTTATCCTACTCTATGCTCCCTCCCTCCCTCTCTCTCTGCTGACTCAAAATAC 73232
Qy 4678 AGGTATATTTAAACATTTATTTGTTTCAAGGACCTTGGATGCTCTCTCTCTCTCTCTCT 4737
Db 73233 AGGTATATTTAAACATTTATTTGTTTCAAGGACCTTGGATGCTCTCTCTCTCTCTCTCT 73292
Qy 4738 GTCTTTCAATTTGGAATAATTTCTACAGCTATCTTCAAGTTTCACTGATCTCTTTCTCTAG 4797
Db 73293 GTCTTTCAATTTGGAATAATTTCTACAGCTATCTTCAAGTTTCACTGATCTCTTTCTCTAG 73352
Qy 4798 TCATATCTAGTGTCTCAACGCTGTGTGAAGAAATCCTTTGCTTTTAAATATCAAGTTTTT 4857
Db 73353 TCATGTCTAGTGTCTCAACGCTGTGTGAAGAAATCCTTTGCTTTTAAATATCAAGTTTTT 73412
Qy 4858 TATTTCTAGCAATTTTCAATCTTGTGTTTCTGTTTCCATCTCTCTACTCACTTTTTT 4917
Db 73413 TATTTCTAGCAATTTTCAATCTTGTGTTTCTGTTTCCATCTCTCTACTCAC-TTTTT 73471
Qy 4918 TTTTTTTTTTTTTTTTTTTTTTTTGAACAGAGTCTCGCTCTGTCACCCAGGCTGGAGTGTAGT 4977
Db 73472 TTTTTTTTTTTTTTTTTTTTTTTTGAACAGAGTCTCGCTCTGTCACCCAGGCTGGAGTGTAGT 73531
Qy 4978 GGGCGATCTCGGCTCACTGGAATTTACAGGTGCCACACCGTGGCTGGCTAAATTTTGTATTT 5037
Db 73532 GGGCGATCTCGGCTCACTGGAATTTACAGGTGCCACACCGTGGCTGGCTAAATTTTGTATTT 73591
Qy 5038 TCCCTCCGAGTGTGGAATTTACAGGTGCCACACCGTGGCTGGCTAAATTTTGTATTT 5097
Db 73592 TCCCTCCGAGTGTGGAATTTACAGGTGCCACACCGTGGCTGGCTAAATTTTGTATTT 73651
Qy 5098 TTTTAGTGGAAACAGGTTTTCAATGTTGGCAGGCTGTCTTGAATTCCTGACCTCAG 5157
Db 73652 TTTTAGTGGAAACAGGTTTTCAATGTTGGCAGGCTGTCTTGAATTCCTGACCTCAG 73711
Qy 5158 GTGATCCACCTGCTCAGCCTCCCAATTTGCTGAATTAAGTGGCAGTGAAGGCACTGCACCC 5217
Db 73712 GTGATCCACCTGCTCAGCCTCCCAATTTGCTGAATTAAGTGGCAGTGAAGGCACTGCACCC 73771

Qy 5218 AGCTCTGCTGACATTTTTTATCTTTTGTGTCATTTTGTCTACTTTTCCATGAAATCCTT 5277
Db 73772 AGCTCTGCTGACATTTTTTATCTTTTGTGTCATTTTGTCTACTTTTCCATGAAATCCTT 73831
Qy 5278 TAAACATAGTAGTATAGTTACTTTTCAATTTCCCTTGTCTGACAGTTCTTGACATTTCAAGTCTA 5337
Db 73832 TAAACATAGTAGTATAGTTACTTTTCAATTTCCCTTGTCTGACAGTTCTTGACATTTCAAGTCTA 73891
Qy 5338 GGTCTGTAAATAGCTTTGTGAGTCTGTTAAACAGCTTTTTTCAATCTTGTCTGTGTGTT 5397
Db 73892 GGTCTGTAAATAGCTTTGTGAGTCTGTTAAACAGCTTTTTTCAATCTTGTCTGTGTGTT 73951
Qy 5398 TGTATTTCTTGATGTATGCGCAAAATATGCTGTGTAATAAATAAATAGATAGATCACTATT 5457
Db 73952 TGTATTTCTTGATGTATGCGCAAAATATGCTGTGTAATAAATAAATAGATAGATCACTATT 74011
Qy 5458 CTATCCAGAAATAGGCACATTTTTTGTGTCAGTCAATTAGTGTGAGGAGGTGTTGGGCA 5517
Db 74012 CTATCCAGAAATAGGCACATTTTTTGTGTCAGTCAATTAGTGTGAGGAGGTGTTGGGCA 74071
Qy 5518 GTCTAGTCACTGCTGAACTAGGTTTTGGATTTGTTGATGCTATATCTTAGAATGCACCA 5577
Db 74072 GTCTAGTCACTGCTGAACTAGGTTTTGGATTTGTTGATGCTATATCTTAGAATGCACCA 74131
Qy 5578 CTTCATTTCACTGCAAGAGTGGCTGCTGCGCTTTGTGATTTCAATGTAGGCTTGAATGCT 5637
Db 74132 CTTCATTTCACTGCAAGAGTGGCTGCTGCGCTTTGTGATTTCAATGTAGGCTTGAATGCT 74191
Qy 5638 ----GGGTTTTTCTTAGTGTCTCCTCAAGTCTCAGATTTTCAAGAGTCTTCTCATATCTG 5693
Db 74192 GGAAGGTTTTTCTTAGTGTCTCCTCAAGTCTCAGATTTTCAAGAGTCTTCTCATATCTG 74251
Qy 5694 TGCACAGAGAGGATCTGACCCATGCTTTTGTGACTCCCAAGTATCAACTGTTGCT 5753
Db 74252 TGCACAGAGAGGATCTGACCCATGCTTTTGTGACTCCCAAGTATCAACTGTTGCT 74311
Qy 5754 TGTATAGCTTGTTCATGAGTAAAGAGGTTGTTTTTTTAGTTTTTATCTTCTCCAGGCTTGGT 5813
Db 74312 TGTATAGCTTGTTCATGAGTAAAGAGGTTGTTTTTTTAGTTTTTATCTTCTCCAGGCTTGGT 74371
Qy 5814 CTTCGGGCTTGAAGTCTTAGACTCCAGGAGTGAATGGAATCCAGTATTTCTCAGTAAT 5873
Db 74372 CTTCGGGCTTGAAGTCTTAGACTCCAGGAGTGAATGGAATCCAGTATTTCTCAGTAAT 74431
Qy 5874 CAGCCCTTCTCCAGTATGTCAGATCTCTGCTTTTGTATCAGTGCAAGATCTCTGGGCTGA 5933
Db 74432 CAGCCCTTCTCCAGTATGTCAGATCTCTGCTTTGTATCAGTGCAAGATCTCTGGGCTGA 74491
Qy 5934 GCTCATTTTCTGCTTCTCGAGTGGCAGACAGCTCTTCTGCTTCCACCTTCTACCAAG 5993
Db 74492 GCTCATTTTCTGCTTCTCGAGTGGCAGACAGCTCTTCTGCTTCCACCTTCTACCAAG 74551
Qy 5994 GCAGTGCATCTTTTCTTGGGCTCTCCCATTTGAATTTATGATTTTCCATATAAGAGAGG 6053
Db 74552 GCAGTGCATCTTTTCTTGGGCTCTCCCATTTGAATTTATGATTTTCCATATAAGAGAGG 74611
Qy 6054 GCTCATGTATCAGAGAAATCTGTGACTTTGTGCCACATACAGAGTCTCTCAGTTCTCTTG 6113
Db 74612 GCTCATGTATCAGAGAAATCTGTGACTTTGTGCCACATACAGAGTCTCTCAGTTCTCTTG 74671
Qy 6114 CCTGCCCCAGTCTTTTGTGAGCAGCTAGTAGAGACCTTGGAGAGGAGGAGGAGG 6173
Db 74672 CCTGCCCCAGTCTTTTGTGAGCAGCTAGTAGAGACCTTGGAGAGGAGGAGGAGG 74731
Qy 6174 CAGTATGAGCTCTTTTGTGCTGCTGATTTGTTTCTCAACTGCTACTCTTGACT 6233
Db 74732 GAGTATGAGCTCTTTTGTGCTGCTGATTTGTTTCTCAACTGCTACTCTTGACT 74791
Qy 6234 TTAAGAAATCAATTAATAATTTTCACTGTTTCTTTTATCTTTTGTGTTTTTTTTTTTTT 6293
Db 74792 TTAAGAAATCAATTAATAATTTTCACTGTTTCTTTTATCTTTTGTGTTTTTTTTTTTTT 74851

QY	6294	TTTTTTTTTTT	TAGATGAGATCTTGGCTCTGTGTCCAGGCTGGAGTGCAATGGTGTGATC	6355
DB	74852	TTTTTTTTTTTT	TAGATGAGATCTTGGCTCTGTGTCCAGGCTGGAGTGCAATGGTGTGATC	74911
QY	6354	TTGGCTTGCT	CTCAACCTCCGGCTCCCGGGTTCAAGGATTCCTCGCCTCAGCTCCCAA	6413
DB	74912	TTGCTTGCT	CAACCTCCGGCTCCCGGGTTCAAGGATTCCTCGCCTCAGCTCCCAA	74971
QY	6414	GTAGTTGGGA	TATACAGTGGCCACCAACCAACCTGGCTAATTTTGTATTTTAGTAGAC	6473
DB	74972	GTAGTTGGGA	TATACAGTGGCCACCAACCAACCTGGCTAATTTTGTATTTTAGTAGAC	75031
QY	6474	ACAGGGTTT	CACCATTTTGGTCAAGCTTGCTCAAACTCCTGACCTCATGATCTGCCGC	6533
DB	75032	ACAGGGTTT	CACCATTTTGGTCAAGCTTGCTCAAACTCCTGACCTCATGATCTGCCGC	75091
QY	6534	CTCAGCCTC	CCAAAGTCTCGGGATTAAGGCATGAGCCACCGCCCGAGCCTCAGCTGTT	6593
DB	75092	CTCAGCCTC	CCAAAGTCTCGGGATTAAGGCATGAGCCACCGCCCGAGCCTCAGCTGTT	75151
QY	6594	CTCTTTTTT	ACCTGCTGGGATGGCTAGTTTCTGTGTCAACTTGAATGGGCCCATGGGATGT	6653
DB	75152	CTCTTTTTT	ACCTGCTGGGATGGCTAGTTTCTGTGTCAACTTGAATGGGCCCATGGGATGT	75211
QY	6654	CCAGATATG	TAATAATAACAGTATTTCTGGGTGTTTCTGTGAGGGTGTCTTCAGAGAGAT	6713
DB	75212	CCAGATATG	TAATAATAACAGTATTTCTGGGTGTTTCTGTGAGGGTGTCTTCAGAGAGAT	75271
QY	6714	TTGCAITTT	GAAATGGTGAATAGTAAGACAGAGGCCCTGTCTAGTAGGGTAGGCATC	6773
DB	75272	TTGCAITTT	GAAATGGTGAATAGTAAGACAGAGGCCCTGTCTAGTAGGGTAGGCATC	75331
QY	6774	ATCCAGTCT	CTGTGAGGACTTGAATAGAAACAAAGGCAGGGGAGGTTCGATTCGCCCT	6833
DB	75332	ATCCAGTCT	CTGTGAGGACTTGAATAGAAACAAAGGCAGGGGAGGTTCGATTCGCCCT	75391
QY	6834	CTCTGTTG	AGCTGAGACATCTATCTGCCCCTGGCACTCCTCGTCTCAGGGGTTCAGA	6893
DB	75392	CTCTGTTG	AGCTGAGACATCTATCTGCCCCTGGCACTCCTCGTCTCAGGGGTTCAGA	75451
QY	6894	CCTGGATT	CTCT - GGTCTCAACCTTGCCCATGCGACACTGTGGACTTCTCAGCGGTCTAT	6952
DB	75452	CCTGGATT	CTCTGGGCTTCCACCTTGCCCATGCGACACTGTGGACTTCTCAGCGGTCTAT	75511
QY	6953	CTAATTAAT	AAATCTCTTCATACACACACACACACACACACACACACACACACACACA	7012
DB	75512	CTAATTAAT	AAATCTCTTCATACACACACACACACACACACACACACACACACACACA	75571
QY	7013	CACACAC	ACCTATGATCTCTCTGTTCTCTGAGAACCATATCTATAACACTGCTTT	7072
DB	75572	CACACAC	ACCTATGATCTCTCTGTTCTCTGAGAACCATATCTATAACACTGCTTT	75631
QY	7073	TATGAGAT	TACCTATCGATTCTGTATTCGCAAAACGTGAAAACAGTTCAATTTTCCAT	7132
DB	75632	TATGAGAT	TACCTATCGATTCTGTATTCGCAAAACGTGAAAACAGTTCAATTTTCCAT	75691
QY	7133	CTCTTCT	CAGAGGCTTGTACCACTATGTTCTCTGATGGGCTCAAGAGTTATGAGT	7192
DB	75692	CTCTTCT	CAGAGGCTTGTACCACTATGTTCTCTGATGGGCTCAAGAGTTATGAGT	75751
QY	7193	TTTTTTTTT	CTCACTGTAGGATGGAATGATTCGTGAAACTTTCATATACCTAAGT	7252
DB	75752	TTTTTTTTT	CTCACTGTAGGATGGAATGATTCGTGAAACTTTCATATACCTAAGT	75811
QY	7253	GGAAA	CTTGTTTGAGGTTATTTTCTACTTACTTTTTTCTGGAAATGGAACACTCTGTA	7312
DB	75812	GGAACT	CTGTTTGAGGTTATTTTCTCTACTTACTTTTTTCTGGAAATGGAACACTCTGTA	75871
QY	7313	TCTAGT	TAAGACATATAACTCAGCTGTGATACCATATGTTGTGTTGAATTTTATTC	7372
DB	75872	TCTAGT	TAAGACATATAACTCAGCTGTGATACCATATGTTGTGTTGAATTTTATTC	75931
QY	7373	TTAGAAAA	TCATCTGTCAAGGTGTTAACTAATGCGAAAGCACTTTAAATAAATCAGCAATCA	7432

Db	75932	TTAGAAAAATCATCTGTCACAGGTGTTAACTAATGGCAAGACATTTAAATAATCAGCAATTCA	75991
QY	7433	TGTATTACAGTGTCTGAAATATCTGACTTTTAAATCTTTACTTTATAAAATGAGAAAATT	7492
Db	75992	TGTATTACAGTGTCTGAAATATCTGACTTTTAAATCTTTACTTTATAAAATGAGAAAATT	76051
QY	7493	GGGCGATGAAAAGTTAACTCTCCTAACCCCGAATTATTACATTTATTAAAGGACAGGACTT	7552
Db	76052	GGGCGATGAAAAGTTAACTCTCCTAACCCCGAATTATTACATTTATTAAAGGACAGGACTT	76111
QY	7553	AGAGGCCAGATATCTTTAAGTCATTAATATTTCTTTGGCTCACGAAATTTGGCAGTATAACCT	7612
Db	76112	AGAGGCCAGATATCTTTAAGTCATTAATATTTCTTTGGCTCACGAAATTTGGCAGTATAACCT	76171
QY	7613	AAAGGTAATACTAGGTGATTTCTTTTATATCAATTAATATGTCAGTTTTCNAATATT	7672
Db	76172	AAAGGTAATACTAGGTGATTTCTTTTATATCAATTAATATGTCAGTTTTCNAATATT	76231
QY	7673	CATAAGTACTACTGTGCAGGGAAGAAACATGCCATACAAAAGATGTAGTCCAGGCCCTTT	7732
Db	76232	CATAAGTACTACTGTGCAGGGAAGAAACATGCCATACAAAAGATGTAGTCCAGGCCCTTT	76291
QY	7733	AGAAACTTTTCATTTAATGGGAACTCAAGAAGTGTACATATAAGGAGGGAAGTAGCAGTA	7792
Db	76292	AGAAACTTTTCATTTAATGGGAACTCAAGAAGTGTACATATAAGGAGGGAAGTAGCAGTA	76351
QY	7793	TGGTACAAGATAATACATACATATCAGTGAATGATTTGCCAAAAAGTGTCTATTGTAGA	7852
Db	76352	TGGTACAAGATAATACATACATATCAGTGAATGATTTGCCAAAAAGTGTCTATTGTAGA	76411
QY	7853	GAAATAATTCATTTCTGCAAAACAGCTGCTGATCTCTACTGAAAAACAGAGGAGGGAAC	7912
Db	76412	GCAATAATTCATTTCTGCAAAACAGCTGCTGATCTCTACTGAAAAACAGAGGAGGGAAC	76471
QY	7913	AGGAGCCCTCGTGGTCAGGATAGAGAGAAAGACCTTTGAGTTTGAGCCTTTGAAACAGTATTT	7972
Db	76472	AGGAGCCCTCGTGGTCAGGATAGAGAGAAAGACCTTTGAGTTTGAGCCTTTGAAACAGTATTT	78531
QY	7973	AAATTTCAAAGGTTTAAGAGAGAGAGCAATTTGAGGAGGGGAGAAATAGTTTCCAGCAAAA	8032
Db	76532	AAATTTCAAAGGTTTAAGAGAGAGAGCAATTTGAGGAGGGGAGAAATAGTTTCCAGCAAAA	76591
QY	8033	TCATGGGTACAAAGATGAACACAGTCAGTAAAGACGACAGCTGCTCGGATGGAGAGGAGG	8092
Db	76592	TCATGGGTACAAAGATGAACACAGTCAGTAAAGACGACAGCTGCTCGGATGGAGAGGAGG	76651
QY	8093	ATTCGCATCATTTGGGATTAAGTCATTTAGACCCCTTGAAAGCCAGGATTCAGTAAAGCCA	8152
Db	76652	ATTCGCATCATTTGGGATTAAGTCATTTAGACCCCTTGAAAGCCAGGATTCAGTAAAGCCA	76711
QY	8153	CAGTCAAGCGACTGCTCGTATGGAAGCTTTATTTTAGARGATTAATCTGGTAGTGACA	8212
Db	76712	CAGTCAAGCGACTGCTCGTATGGAAGCTTTATTTTAGARGATTAATCTGGTAGTGACA	76771
QY	8213	TGTGCCAAAACTGAATAGGTAGAAATCAGATGCGAGAGCCCGAGTTAGAACTTAAGCTCTG	8272
Db	76772	TGTGCCAAAACTGAATAGGTAGAAATCAGATGCGAGAGCCCGAGTTAGAACTTAAGCTCTG	76831
QY	8273	GTGCAGTAAATCGCAGGATTTGAGGCAATAACACCAAACCTACAGTATCAACAGATATGGAT	8332
Db	76832	GTGCAGTAAATCGCAGGATTTGAGGCAATAACACCAAACCTACAGTATCAACAGATATGGAT	76891
QY	8333	GTTTGAACCGACGGTTTAAAGGAAAAATGATGGTATTTTGGTAAATTTATTAGATAATCCAG	8392
Db	76892	GTTTGAACCGACGGTTTAAAGGAAAAATGATGGTATTTTGGTAAATTTATTAGATAATCCAG	76951
QY	8393	GGCCATGGAATGAGAGGGGAAAAATGACTAAACATAGTCATCAAAATGGTTTTCTTTAATGA	8452
Db	76952	GGCCATGGAATGAGAGGGGAAAAATGACTAAACATAGTCATCAAAATGGTTTTCTTTAATGA	77011
QY	8453	ATCTGAATTTTGGTGTAGAGCAACATTTCTTAGGCCCTTGCTAGTTGGTACAGCTGAC	8512

Db 81392 TGGAGCTGTGATATTACAAACGTGAAAGATGACGAGCACTTCAGTGAGTA 81451
Qy 12888 AACAAAGGCTTTCAATCAGCATG-ATTTATTGACTGCC-AAAATCGGGCTG-CTTCCTG 12944
Db 81452 AACAAAGGCTTTCAATCAGCATGATTTATTGACTGCCCTGACTCTGGGCTGCCTTCCTG 81511
Qy 12945 TCTGTGGTTCAAGGAGAGCATAGTCTACAGAACGAGACCTGGTACTCTGGAGTTAG 13004
Db 81512 TCTGTGGTTCAAGGAGAGCATAGTCTACAGAACGAGACCTGGTACTCTGGAGTTAG 81571
Qy 13005 ACTTAAGCCACCCCGGCTCTTGAATGGGCAATATTTCCCTTCATTCCTGTGTTTTAGG 13064
Db 81572 ACTTAAGCCACCCCGGCTCTTGAATGGGCAATATTTCCCTTCATTCCTGTGTTTTAGG 81631
Qy 13065 GACAGAAAGATGAGTAATGCAGTGATACATGCTGGAAATGTTTTATTCACCTACCCGAAGC 13124
Db 81632 GACAGAAAGATGAGTAATGCAGTGATACATGCTGGAAATGTTTTATTCACCTACCCGAAGC 81691
Qy 13125 TGCCTCTCACTTAACAATCCATGAAAGAAACAAGATGATATATACTTTTCTAAATTTG 13184
Db 81692 TGCCTCTCACTTAACAATCCATGAAAGAAACAAGATGATATATACTTTTCTAAATTTG 81751
Qy 13185 TGAATGCTTTGTTTTATTGTTTCCGGTTAAAGAGAGAGTGCGCATTTGAATGTTTTGTTG 13244
Db 81752 TGAATGCTTTGTTTTATTGTTTCCGGTTAAAGAGAGAGTGCGCATTTGAATGTTTTGTTG 81811
Qy 13245 GTTTGTTTCTTCTTCAATAAGNAGCATCTTAATATAGTACTGAGCATCTGCCAT 13304
Db 81812 GTTTGTTTCTTCTTCAATAAGNAGCATCTTAATATAGTACTGAGCATCTGCCAT 81871
Qy 13305 TTTCAAAATTTACAAGTTTCGATCATTTGCTAAATTTACAGATCCCAATCTGTGCTCT 13364
Db 81872 TTTCAAAATTTACAAGTTTCGATCATTTGCTAAATTTGTAAGATCCCAATCTGTGCTCT 81931
Qy 13365 GCATATTTGCAATTTATAAGCAGAGCAGTACGAGTCTTCTAATGCAATCCCTCC 13424
Db 81932 GCATATTTGCAATTTATAAGCAGAGCAGTACGAGTCTTCTAATGCAATCCCTCC 81991
Qy 13425 AAATGATGAGATTTAGATTTGCTTCCCTATTGTTTCAATGCTTAAAGGCTTAA 13484
Db 81992 AAATGATGAGATTTAGATTTGCTTCCCTATTGTTTCAATGCTTAAAGGCTTAA 82051
Qy 13485 AGGATCATTTGATTTAAATTTAATTTAATTTGTFACAGCAGGTGAGTCTCTTTCTTTTAA 13544
Db 82052 AGGATCATTTGATTTAAATTTAATTTAATTTGTFACAGCAGGTGAGTCTCTTTCTTTTAA 82111
Qy 13545 GGAAGAACCTTCAGGGCAATTCCTTTAGTTTAAATGTTAAATCTCATTTTCTTTGA 13604
Db 82112 GGAAGAACCTTCAGGGCAATTCCTTTAGTTTAAATGTTAAATCTCATTTTCTTTGA 82171
Qy 13605 AAATAAGAAGTTAAAGCTGATTTACACAAGCTCTCAAGCTCTCAAGCTGAGTCTTCAATTTGTT 13664
Db 82172 AAATAAGAAGTTAAAGCTGATTTACACAAGCTCTCAAGCTCTCAAGCTGAGTCTTCAATTTGTT 82231
Qy 13665 TTTAAACCACTAGGAATGTTTGAATCTAATGAACATTTACTGCTGAATTTGGCTGA 13724
Db 82232 TTTAAACCACTAGGAATGTTTGAATCTAATGAACATTTACTGCTGAATTTGGCTGA 82291
Qy 13725 AATTGCTGGGCTGGAATATTTGTTAATCTTCACATGATTTCCAGTGTGTTGTTATTATT 13784
Db 82292 AATTGCTGGGCTGGAATATTTGTTAATCTTCACATGATTTCCAGTGTGTTGTTATTATT 82351
Qy 13785 TTTCTTTTCTTTTGTGACCGATATAGATGAAGCAGAGCAGAGGCAATCCATG 13844
Db 82352 TTTCTTTTCTTTTGTGACCGATATAGATGAAGCAGAGCAGAGGCAATCCATG 82411
Qy 13845 TGTAAATAGAAAAGGCGAGCTGAATTTGTTGCTGTTTTTGAATTTAAAGCTGGTTTTTC 13904
Db 82412 TGTAAATAGAAAAGGCGAGCTGAATTTGTTGCTGTTTTTGAATTTAAAGCTGGTTTTTC 82471
Qy 13905 GATTAAATTCAGTAAATGGTCCAGGACTATAAATGTTGAAATTTTACCCTGTTGATTT 13964
Db 82472 AATTAAATTCAGTAAATGGTCCAGGACTATAAATGTTGAAATTTTACCCTGTTGATTT 82531

Qy 13965 AAATTTTAGTCTTATT-----CTTTTTTTTTTTTTTTGATGGTTTACATTTTCC 14012
Db 82532 AAATTTTAGTCTTATTGTTTTTTTTTTTGGTTTTTTTTTTTGGTTTACATTTTCC 82591
Qy 14013 CCATGGAAAGCAGTATGTCTGCGCATGATTCATCATGTGTAAACATCTCGGGTTATTT 14072
Db 82592 CCATGGAAAGCAGTATGTCTGCGCATGATTCATCATGTGTAAACATCTCGGGTTATTT 82651
Qy 14073 TGTGTTGTGTTATGTTTCAGAAAGCGAATGCCAAATAAAGAGTGGTTTGTGATGCTA 14132
Db 82652 TGTGTTGTGTTATGTTTCAGAAAGCGAATGCCAAATAAAGAGTGGTTTGTGATGCTA 82711
Qy 14133 GTGTGCTTCTCTTTAAACAATCAAAGGCTTTTATTAAATCCACTTAATGGGACACTGCAG 14192
Db 82712 GTGTGCTTCTCTTTAAACAATCAAAGGCTTTTATTAAATCCACTTAATGGGACACTGCAG 82771
Qy 14193 AAATTTAAAAATGGAAAGTCCCATCCACAGAGGAGGTACTATGATGTAAAGTTTATG 14252
Db 82772 AAATTTAAAAATGGAAAGTCCCATCCACAGAGGAGGTACTATGATGTAAAGTTTATG 82831
Qy 14253 GTGGGGATTAATAGAGTGATCATATAATTTATGAGCTAAACCGGAGGCACTTTTTTTTT 14312
Db 82832 GTGGGGATTAATAGAGTGATCATATAATTTATGAGCTAAACCGGAGGCACTTTTTTTTT 82891
Qy 14313 TGAGATCGAGTCTCACTGTTGCTAGCTGGAGTGCAGTGAACGTGATCAAGTCACTGCT 14372
Db 82892 TGAGATCGAGTCTCACTGTTGCTAGCTGGAGTGCAGTGAACGTGATCAAGTCACTGCT 82951
Qy 14373 AACCTCGGCTCCCGGGTTCAGGGATTCATGCTCAGCTCCCTGAGTGGAGTGGGACT 14432
Db 82952 AACCTCGGCTCCCGGGTTCAGGGATTCATGCTCAGCTCCCTGAGTGGAGTGGGACT 83011
Qy 14433 ATAGGCCCCCACCACCATGCCCCAGCTAAATTTTTTGTGTTTTTTAGAGATGGGGTTTCA 14492
Db 83012 ATAGGCCCCCACCACCATGCCCCAGCTAAATTTTTTGTGTTTTTTAGAGATGGGGTTTCA 83071
Qy 14493 CATGTTGGCCAGGCTGTCTCAAACTCCTGACCTCAGTGTATCCGCCACCTCGACCTCC 14552
Db 83072 CATGTTGGCCAGGCTGTCTCAAACTCCTGACCTCAGTGTATCCGCCACCTCGACCTCC 83131
Qy 14553 TAAACTCTCGGATTAAGCCGTAAGCCACCATGCTGCGCCAGAGACACTTTTGAGAGT 14612
Db 83132 TAAACTCTCGGATTAAGCCGTAAGCCACCATGCTGCGCCAGAGACACTTTTGAGAGT 83191
Qy 14613 GAAGAGAAAGCTGAGATAATTTCACTGATCTACAACTGGGACCATCCAGGCAAGCCAGA 14672
Db 83192 GAAGAGAAAGCTGAGATAATTTCACTGATCTACAACTGGGACCATCCAGGCAAGCCAGA 83251
Qy 14673 TGCCATTTACCATAGCTAGAAAGCTTCCCAAGGTCTCATTTACCTTGGTATATAGCAAT 14732
Db 83252 TGCCATTTACCATAGCTAGAAAGCTTCCCAAGGTCTCATTTACCTTGGTATATAGCAAT 83311
Qy 14733 TCTTTCTTTTGAATTTCTGGAATTTCTGTAAGTCAATGAGGTAGCTCTGTGCCAAGAGCA 14792
Db 83312 TCTTTCTTTTGAATTTCTGTAAGTCAATGAGGTAGCTCTGTGCCAAGAGCA 83370
Qy 14793 ATATGGTAGAATTTCTAATTTTTCAGGCAG-ACACACTTTTCTGCAATTTGAGCAGTAA 14851
Db 83371 ATATGGTAGAATTTCTAATTTTTCAGGCAGTACACACTTTTCTGCAATTTGAGCAGTAA 83430
Qy 14852 AGGAGGTTCAGGCGAGAGCAAAACCATCTGGGACTCGAAGAGGCAATAAACGTCTAAT 14911
Db 83431 AGGAGGTTCAGGCGAGAGCAAAACCATCTGGGACTCGAAGAGGCAATAAACGTCTAAT 83490
Qy 14912 GCACCTGATGTAGTGTGTAATTTGTTATCAGTAAAGTCTTTTCATTAATAATAAC 14971
Db 83491 GCACCTGATGTAGTGTGTAATTTGTTATCAGTAAAGTCTTTTCATTAATAATAAC 83550
Qy 14972 TTATCATTTGTAGGAGGCAAGAAATCGTGGAAAGCTGGGATTCAGGTTGCCTGTGGCT 15031
Db 83551 TTATCATTTGTAGGAGGCAAGAAATCGTGGAAAGCTGGGATTCAGGTTGCCTGTGGCT 83610

QY	15032	TTAATTCGGAATCAGAAATATTAGTCAAGGATATCAGTCTATGAAGTAAGTTTCAATG	15091	Db	84691	ATACACATATATACATACATAAACAATCTCGCATTTATACCAATTCATTTGTAAACCCATC	84750
Db	83611	TTAATTCGGAATCAGAAATATTAGTCAAGGATATCAGTCTATGAAGTAAGTTTCAATG	83670	QY	16142	TTCCCTAAAACTGTCTCATAAAGAGTCTCTTTTCCCTGTACCTATGCAATGTAAGTA	16201
QY	15092	TTATATGCCACAAGATGACGCTGCTCTATTTTCACTTCCAGTAATTCCTCTCTGAATTAAT	15151	Db	84751	TTCCCTAAAACTGTCTCATAAAGAGTCTCTTTTCCCTGTACCTATGCAATGTAAGTA	84810
Db	83671	TTATATGCCACAAGATGACGCTGCTCTATTTTCACTTCCAGTAATTCCTCTCTGAATTAAT	83730	QY	16202	GCAAAACACACATTTCTTTTGGGTCCCATAAACATTCCTCTGTAGTTTGCCTTTAACAGTCT	16261
QY	15152	ACACCTTAAAAATAGCTGACGCTTCTCAAACTGTGAGAAATCGTATGCTGCTGCTAC	15211	Db	84811	GCAAAACACACATTTCTTTTGGGTCCCATAAACATTCCTCTGTAGTTTGCCTTTAACAGTCT	84870
Db	83731	ACACCTTAAAAATAGCTGACGCTTCTCAAACTGTGAGAAATCGTATGCTGCTGCTAC	83790	QY	16262	TTGATGTGAAATTTTACGTGTTTCTGTCTTAACTTGCCTGTCTCCGCTACATGAGTTTG	16321
QY	15212	ACTTTC--TTTTCCTGGAAGGCTTTTGGAGTCTTTCAAGAACTCAATTCAGCAA	15269	Db	84871	TTGATGTGAAATTTTACGTGTTTCTGTCTTAACTTGCCTGTCTCCGCTACATGAGTTTG	84930
Db	83791	ACTTTCCTTTTCTGAGGCTCTTTGAGTCTTTTCAAGAACTCAATTCAGCAA	83850	QY	16322	GCTCTGCTCCTAGTCTGCACTTTCACCCCATCTTGCCTTGCCTTGCCTTGCCTTGCCT	16381
QY	15270	CAATTAAGGGGCTTAAGGTATAAGAGCTGTGCAAGATGCTCTCTGAGACACAAAGAGGA	15329	Db	84931	GCTCTGCTCCTAGTCTGCACTTTCACCCCATCTTGCCTTGCCTTGCCTTGCCTTGCCT	84990
Db	83851	CAATTAAGGGGCTTAAGGTATAAGAGCTGTGCAAGATGCTCTCTGAGACACAAAGAGGA	83910	QY	16382	ACCACTGCTCATCTTTCTGCTGCGACAACTCCAGTCCAGGCTCCAGGCTCCCTCTCTCTCT	16441
QY	15330	GGTCAAGCCCTCCCTTCAGGACCTCTCTATATATAGAGGAGAGAGAGAGAAACAC	15389	Db	84991	ACCACTGCTCATCTTTCTGCTGCGACAACTCCAGTCCAGGCTCCAGGCTCCCTCTCTCTCT	85050
Db	83911	GGTCAAGCCCTCCCTTCAGGACCTCTCTATATATAGAGGAGAGAGAGAGAAACAC	83970	QY	16442	GGACTCTCTGCGGGAGTTCCTTCTCTCTGCTGCACTGAGTCTATTTCTCGCACAACTGGCA	16501
QY	15390	TAATACACATAGGTAGGTGCAATAAAGGGTACATACATTTAAAGCCAGGTGCTAGGTGT	15449	Db	85051	GGACTCTCTGCGGGAGTTCCTTCTCTCTGCTGCACTGAGTCTATTTCTCGCACAACTGGCA	85110
Db	83971	TAATACACATAGGTAGGTGCAATAAAGGGTACATACATTTAAAGCCAGGTGCTAGGTGT	84030	QY	16502	TAGTAAAGTGAAGTCTGCGAAGAGGCAAGTTTGCAGTCCAGGAAATGAAGACTCTGTC	16561
QY	15450	AAGAAGATTGTAAACATGAGAAATTTTCTGATGTTTGAATATCTTATTAATTTTAAAAA	15509	Db	85111	GAGTAAAGTGAAGTCTGCGAAGAGGCAAGTTTGCAGTCCAGGAAATGAAGACTCTGTC	85170
Db	84031	AAGAAGATTGTAAACATGAGAAATTTTCTGATGTTTGAATATCTTATTAATTTTAAAAA	84090	QY	16562	TTGTGCACATCTCTGGGTTTGACGGGTGCTGATATCGATGATCGATGATCGATGATG	16621
QY	15510	TTAAATGGGAGATACATATATATGTTATGTTATGTTATATATGTTATGTTATGTTATG	15569	Db	85171	TTGTGCACATCTCTGGGTTTGACGGGTGCTGATATCGATGATCGATGATCGATGATG	85230
Db	84091	TTAAATGGGAGATACATATATATGTTATGTTATGTTATATGTTATGTTATGTTATG	84150	QY	16622	TCAAGGCTTAAAGGAGAGATAGGGCTGATGATCTGAGATTCATCAGTGTGTGCTGATG	16681
QY	15570	ACATATACATAAATATACATAAATATGTTATATGTTATATGTTATATGTTATATGTT	15629	Db	85231	TCAAGGCTTAAAGGAGAGATAGGGCTGATGATCTGAGATTCATCAGTGTGTGCTGATG	85290
Db	84151	ACATATACATAAATATACATAAATATGTTATATGTTATATGTTATATGTTATATGTT	84210	QY	16682	TTTAAACCCAGGGACAGGATTAAGAGTTATTCAGGAGAGAGGTAGATAAAGAGCTA	16741
QY	15630	ATATATGTTATATACATAAATATGTTATATGTTATATGTTATATGTTATATGTTATAT	15689	Db	85291	TTTAAACCCAGGGACAGGATTAAGAGTTATTCAGGAGAGAGGTAGATAAAGAGCTA	85350
Db	84211	ATATATGTTATATACATAAATATGTTATATGTTATATGTTATATGTTATATGTTATAT	84270	QY	16742	AATGGCTTCTGGGTCCTTAGTCAATTCAAAATCGGACCTCTGAGGACAGGAGAAAGCCAG	16801
QY	15690	ATGTTATATAGACATAAATATGTTATATGTTATATGTTATATGTTATATGTTATATG	15749	Db	85351	AATGGCTTCTGGGTCCTTAGTCAATTCAAAATCGGACCTCTGAGGACAGGAGAAAGCCAG	85410
Db	84271	ATGTTATATAGACATAAATATGTTATATGTTATATGTTATATGTTATATGTTATATG	84330	QY	16802	AAAGAGTAGATTCCTGGGACTCAGCGGATAAAGACTTTCAAAAGTGGGGCTGGCCAGT	16861
QY	15750	GTATATAGACATAAATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTAT	15809	Db	85411	AAAGAGTAGATTCCTGGGACTCAGCGGATAAAGACTTTCAAAAGTGGGGCTGGCCAGT	85470
Db	84331	GTATATAGACATAAATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTAT	84390	QY	16862	GCTCTGAAGAAAGTAGCAGGACCGGAAACAGAGGGTAACTGTTGGACCTGGAGAACTTG	16921
QY	15810	ATAGACATAAATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATG	15869	Db	85471	GCTCTGAAGAAAGTAGCAGGACCGGAAACAGAGGGTAACTGTTGGACCTGGAGAACTTG	85530
Db	84391	ATAGACATAAATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATG	84450	QY	16922	AATTGAAATTTTAAAGTTGTTAACTTAAAGAGCAATTTTAGATACCTTTTGAATTT	16981
QY	15870	ACATAAATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTAT	15929	Db	85531	AATTGAAATTTTAAAGTTGTTAACTTAAAGAGCAATTTTAGATACCTTTTGAATTT	85590
Db	84451	ACATAAATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTAT	84510	QY	16982	ATTTGCAAGATTTTCTGTTGTTATGTTATTCAGGCAAGGAGGACAGAAAAGTAAAAA	17041
QY	15930	AAATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATG	15989	Db	85591	ATTTGCAAGATTTTCTGTTGTTATGTTATTCAGGCAAGGAGGACAGAAAAGTAAAAA	85650
Db	84511	AAATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATG	84570	QY	17042	ATACTTACTGAACAGTTTACTGCACTGCTGCACTGTAAACCCCTGTTTAAATTCACGGC	17101
QY	15990	ATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTAT	16029	Db	85651	ATACTTACTGAACAGTTTACTGCACTGCTGCACTGTAAACCCCTGTTTAAATTCACGGC	85710
Db	84571	ATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTAT	84630	QY	17102	AACCTTACTAGATGTTGTTCTCATCTCCCATCTTACAGATGAGGATAGAGGTCAGCTA	17161
QY	16030	-----TGTATATGACATAAATATGTTATATGTTATATGTTATATGTTATATGTTAT	16081	Db	85711	AACCTTACTAGATGTTGTTCTCATCTCCCATCTTACAGATGAGGATAGAGGTCAGCTA	85770
Db	84631	ATATATGTTATATGACATAAATATGTTATATGTTATATGTTATATGTTATATGTTAT	84690	QY	17162	GATTAAACAGTTTGCCTCAGGTTACACCACTGTTAACTAGAGCTAGAGTTTGAACCC	17221
QY	16082	ATACACATATATACATACATAAACAATTCCTGCATTTATACCATTCCTGTTTGAACCCATC	16141				

Db 85771 GATTAGCAGCTTTGCCCTCAGGTTACACCACTGGTTAACTAGCTAGGATTTTGAACCC 85830
Qy 17222 GGATGGGCTGATCCAGAGACTGATGCTTTAAATCGCTAGACTGGTCTCACAGAGACTG 17281
Db 85831 GGATGGGCTGATCCAGAGACTGATGCTTTAAATCGCTAGACTGGTCTCACAGAGACTG 85890
Qy 17282 GGAACCAAAATTAATAAATAAATAAGGAGCCCTGGCTAGCAAAATTAGCAGTTG 17341
Db 85891 GGACCAAAATTAATAAATAAATAAGGAGCCCTGGCTAGCAAAATTAGCAGTTG 85950
Qy 17342 TTCCAGACAGATGTGAAAGGAAAGCAAGCAGAGGGAAGTCACTGTACAGAGAGAGAG 17401
Db 85951 TTCCAGACAGATGTGAAAGGAAAGCAAGCAGAGGGAAGTCACTGTACAGAGAGAGAG 86010
Qy 17402 ACCATGACAGCAGACAGCTGAGCTGTAAAGTGGCTGGCGATCTAGCCCTGAAATA 17461
Db 86011 ACCATGACAGCAGACAGCTGAGCTGTAAAGTGGCTGGCGATCTAGCCCTGAAATA 86070
Qy 17462 CTCCAGAGAGGAGGCTCACGCTGTAAATCCAGCACTTTGGAGGCGGAGGTGGCAG 17521
Db 86071 CTCCAGAGAGGAGGCTCACGCTGTAAATCCAGCACTTTGGAGGCGGAGGTGGCAG 86130
Qy 17522 ATCAGCTGAGGCTGAGAGTTGAGACAGCTGGCCGAAATCCGCTCTACTA 17581
Db 86131 ATCAGCTGAGGCTGAGAGTTGAGACAGCTGGCCGAAATCCGCTCTACTA 86190
Qy 17582 AAAATACAAAATTTAGCCGAGCATGCTGACAGCAGCTGTAAATCCAGCACTTTGAGTTGG 17641
Db 86191 AAAATACAAAATTTAGCCGAGCATGCTGACAGCAGCTGTAAATCCAGCACTTTGAGTTGG 86250
Qy 17642 CTGAGTCAGAGAAATAGCTGGATCCGGAAGTGGAGTTGTAGTAAGCAAGATTGGCC 17701
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Qy 17762 AAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 17821
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Qy 17882 GAAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 17941
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Qy 17942 TAGGCTTTGAGAACTCAGTCCCTTTTATGAGAAACAAATGCTTACACTCTCAATG 18001
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Qy 18002 TTATTGTATCCAAAGTTATCAATATACCTTAATCACTTAGTACTGAAATCTGGCATATAG 18061
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Qy 18301 GTGGTGGCTGAGCTGGGGTAACTCCGTAACTGTAAATGGAACCTAAACAAATACATGAA 18360
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Qy 18481 CGTAGGCTTTCCACTTGCACCTACAGCTTTACAAATGTTGGACTATCTTCAGATGGCACCT 18540
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Qy 18541 CCTTGCATTTGCTCAGCAGAGAGCTTTTCCCTCCAGCTTTCTAGGTGATTAATAT 18600
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Qy 18661 CTAAATTCGAAAGTCACTTTTACATGATTTTCACTATGAAATAGGCAAGTAGA 18720
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Db 87751 CCTCTCAAGGTTTACCCCAATTTCTCAGTTCTCTCAGGAAAGCCAAATGAATTTGA 87810
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Db 87871 TGTCTCTCTGTAACAACTACTCTTCCAGACTACTGAGATTTGATATGTTCTCCACAG 87930
Qy 19321 CAAGTAAACACAGAAATGGCTGCCCAATTTCCAAATCCCTGAACTGAGTGAAGAAATCA 19380
Db 87931 CAAGTAAACACAGAAATGGCTGCCCAATTTCCAAATCCCTGAACTGAGTGAAGAAATCA 87990

QY	19381	GAATTATATAGGGGATTCAACAGAGCTGGCTACGGATGTGCCAGTGGTCAGATACCTTTG	19440	Db	89071	CCCACTCAGCCTCCCAAGCACCTGGGATTACAGCATAGCCCGTGGCCAGCCTGTT	89130
Db	87991	GAATTATATAGGGGATTCAACAGAGCTGGCTACGGATGTGCCAGTGGTCAGATACCTTTG	88050	QY	20520	TTCTCAGATCCTGTA-TTTGTTTCTGAAGCCTTCATTTCTATCTTCTTATTCATTTTGA	20578
QY	19441	CTCATATACGCGAGGTGCTGCTCTCTAGCAACTGCTCACTGCTTCATTTCTCTGCTCTGG	19500	Db	89131	TTCTCAGATCCTGTA-TTTGTTTCTGAAGCCTTCATTTCTATCTTCTTATTCATTTTGA	89190
Db	88051	CTCATATACGCGAGGTGCTGCTCTCTAGCAACTGCTCACTGCTTCATTTCTCTGCTCTGG	88110	QY	20579	AGTAGTACACCTAGTAAAGTTTAAACATCAAAATATCTTTGAAAAATCCCTGGTTC	20638
QY	19501	TCCTTAAATACTGCTTTCTCAGCTCAATTTGGCTTTCTTCCCTCTGGCAGTACGTTTCT	19560	Db	89191	AGTAGTACACCTAGTAAAGTTTAAACATCAAAATATCTTTGAAAAATCCCTGGTTC	89250
Db	88111	TCCTTAAATACTGCTTTCTCAGCTCAATTTGGCTTTCTTCCCTCTGGCAGTACGTTTCT	88170	QY	20639	TTTCTTATTCCTACAAAAATATGTTTCAGTATAGCTGATGTTATGTTCTTTTCAAAATATT	20698
QY	19561	TTGGGTCAAAACAGCAATGATTTCTTAGAATCACTGGTACTCAAAAGGAGCTACAAGACA	19620	Db	89251	TTTCTTATTCCTACAAAAATATGTTTCAGTATAGCTGATGTTATGTTCTTTTCAAAATATT	89310
Db	88171	TTGGGTCAAAACAGCAATGATTTCTTAGAATCACTGGTACTCAAAAGGAGCTACAAGACA	88230	QY	20699	CATTCTCTATCTCAGAAATTTATCTCAATGCTTAATGTTTATGTAATAGTCTTCACTCTT	20758
QY	19621	TTGGGATCCACTTCCACTCTCTTGGAAAAACAATTTTATGGAAGCAAGGTTGCCATAG	19680	Db	89311	CATTCTCTATCTCAGAAATTTATCTCAATGCTTAATGTTTATGTAATAGTCTTCACTCTT	89370
Db	88231	TTGGGATCCACTTCCACTCTCTTGGAAAAACAATTTTATGGAAGCAAGGTTGCCATAG	88290	QY	20759	GTCTATCCAGTTTCTGGTCTCTTATTTCACTCTAAGTCTAAGTGGCTATTAGAAATAAGAG	20818
QY	19681	TGCTCTTTGAGGTGTTTGTCTAGCCAGCCCAAGCTTTTGCTTCAACACATGAATTA	19740	Db	89371	GTCTATCCAGTTTCTGGTCTCTTATTTCACTCTAAGTCTAAGTGGCTATTAGAAATAAGAG	89430
Db	88291	TGCTCTTTGAGGTGTTTGTCTAGCCAGCCCAAGCTTTTGCTTCAACACATGAATTA	88350	QY	20819	CTTGTAAACAGATTCTTTCTCCAAATATGTTCTTTTGAATGCTGATCCAGTGAACAAT	20878
QY	19741	GAGAGCTTCAGAAACAAGATCCACATTTTCAATGGCTCACCCAACTGGATAAAGAACAA	19800	Db	89431	CTTGTAAACAGATTCTTTCTCCAAATATGTTCTTTTGAATGCTGATCCAGTGAACAAT	89490
Db	88351	GAGAGCTTCAGAAACAAGATCCACATTTTCAATGGCTCACCCAACTGGATAAAGAACAA	88410	QY	20879	GTTAACTGTTTGTGTTTCTTCAATACATTCACAGAACATGCTGACTCTCTCTCTCTGAA	20938
QY	19801	TTGCCATATCTCAATGACCACTTTT-TCAGTGGGATGGTAGATGCTGGAATGGGTAC	19859	Db	89491	GTTAACTGTTTGTGTTTCTTCAATACATTCACAGAACATGCTGACTCTCTCTCTCTGAA	89550
Db	88411	TTGCCATATCTCAATGACCACTTTT-TCAGTGGGATGGTAGATGCTGGAATGGGTAC	88470	QY	20939	AGCAATGCCCAAGCACAGCATTGTTAGATAGTATGTACGCAACAGGACATGGGTGCATA	20998
QY	19860	AGCAATGCCCAACCAACTTTTGCAAAAAAGGCTGGAGGCTCTGACTGGGGACCTTAATA	19919	Db	89551	AGCAATGCCCAAGCACAGCATTGTTAGATAGTATGTACGCAACAGGACATGGGTGCATA	89610
Db	88471	AGCAATGCCCAACCAACTTTTGCAAAAAAGGCTGGAGGCTCTGACTGGGGACCTTAATA	88530	QY	20999	GCAAAAACTAGAAAGAGGAGGACCTTCTTAGCAATGGGTGATATGGTCCCTGGACTTA	21058
QY	19920	TGCAAAAGTTGATAGGCTCTTCAATGAGAAATATGAACCCCGTGTATGGATATAGCTAAG	19979	Db	89611	GCAAAAACTAGAAAGAGGAGGACCTTCTTAGCAATGGGTGATATGGTCCCTGGACTTA	89670
Db	88531	TGCAAAAGTTGATAGGCTCTTCAATGAGAAATATGAACCCCGTGTATGGATATAGCTAAG	88590	QY	21059	GACTCCAAAGGCTCGTAGAGTGAACACACATCGTCCATACCCAGGAAGCACACAGGTGG	21118
QY	19980	GGTTGGCTTTATGTTTCTTCAATCTTCAAAACCTGGTAGAATAGCTTGTGTTCC	20039	Db	89671	GACTCCAAAGGCTCGTAGAGTGAACACACATCGTCCATACCCAGGAAGCACACAGGTGG	89730
Db	88591	GGTTGGCTTTATGTTTCTTCAATCTTCAAAACCTGGTAGAATAGCTTGTGTTCC	88650	QY	21119	GATGAAAGAGCTGTGCTTAATGAAACCTTCACGCTGGAGGTGGAGGAGCTGGAGCTG	21178
QY	20040	TTTAAAAATGTCACAAATGCAATTTATGATGCTGTATAGTAATCAACATCATGCT	20099	Db	89731	GATGAAAGAGCTGTGCTTAATGAAACCTTCACGCTGGAGGTGGAGGAGCTGGAGCTG	89790
Db	88651	TTTAAAAATGTCACAAATGCAATTTATGATGCTGTATAGTAATCAACATCATGCT	88710	QY	21179	CAAGAACTCAGAGCTGCCTTACCCAGACCCAGGAGCCAGGAGGCTTTCTCGAGGAACA	21238
QY	20100	CCATGAAATGCTTCAGAACCCCAATATAGGAGATTTTTCAGCATGCTGTCACAAAGAG	20159	Db	89791	CAAGAACTCAGAGCTGCCTTACCCAGACCCAGGAGCCAGGAGGCTTTCTCGAGGAACA	89850
Db	88711	CCATGAAATGCTTCAGAACCCCAATATAGGAGATTTTTCAGCATGCTGTCACAAAGAG	88770	QY	21239	GCCTCTGAACCTGCCAGCTGATAGAGGAGCTTACCTCAACTCTTCTGTTCTCCAGGGCT	21298
QY	20160	AGGCCATTTTCAGTGTGAAATTTCTCAGAGAATATTTGATTTATGTTTCTCAGATCTTT	20219	Db	89851	GCCTCTGAACCTGCCAGCTGATAGAGGAGCTTACCTCAACTCTTCTGTTCTCCAGGGCT	89910
Db	88771	AGGCCATTTTCAGTGTGAAATTTCTCAGAGAATATTTGATTTATGTTTCTCAGATCTTT	88830	QY	21299	GCTTTTCCAGCTCCATTTATTTGGCACTGAAAGTTTGAATACCTTCAGGGGCCGGAAGGCT	21358
QY	20220	TTATTTTATTTTGTGAAACAGAGTCTCATTGTCACCCAGGCTGGAGTACAGTGGC	20279	Db	89911	GCTTTTCCAGCTCCATTTATTTGGCACTGAAAGTTTGAATACCTTCAGGGGCCGGAAGGCT	89970
Db	88831	TTATTTTATTTTGTGAAACAGAGTCTCATTGTCACCCAGGCTGGAGTACAGTGGC	88890	QY	21359	GCCAGGTCTCTTCTCTGCAGAGCAATCACACCAACCTCCAAAGGGCTTAGGAAAGGGCTG	21418
QY	20280	TGTGGTCTGGCTCAGTGCACCTCTGCCCTCCAGGTTCAAGGATTTCTCTGTACGTT	20339	Db	89971	GCCAGGTCTCTTCTCTGCAGAGCAATCACACCAACCTCCAAAGGGCTTAGGAAAGGGCTG	90030
Db	88891	TGTGGTCTGGCTCAGTGCACCTCTGCCCTCCAGGTTCAAGGATTTCTCTGTACGTT	88950	QY	21419	TCATCATCTCTACTCAGAAACTGGTTTCACTGGAAGGAGCTCAGGGGCCACTGAATACATC	21478
QY	20340	CCCGAATAGCTGGATPACAGGCGCATGCAACCAAGCTCAATTTTGTATTTTGTAGTA	20399	Db	90031	TCATCATCTCTACTCAGAAACTGGTTTCACTGGAAGGAGCTCAGGGGCCACTGAATACATC	90090
Db	88951	CCCGAATAGCTGGATPACAGGCGCATGCAACCAAGCTCAATTTTGTATTTTGTAGTA	89010	QY	21479	CTGGCAGTTTTCAGAAAGGGCTTCTGACTCAAGGATGTTTCCATCTTTTCCAGGTGCG	21538
QY	20400	GAGACAGATTTCCGCAATGTTACCCAGGCTGCTTGAATCTCTGACTTCAAGTATCA	20459	Db	90091	CTGGCAGTTTTCAGAAAGGGCTTCTGACTCAAGGATGTTTCCATCTTTTCCAGGTGCG	90150
Db	89011	GAGACAGATTTCCGCAATGTTACCCAGGCTGCTTGAATCTCTGACTTCAAGTATCA	89070	QY	21539	CTTTTCTCTCTCTCTTAGAGTTTGGAGACGCAATGTGCTGAGAAGTCAACCTTTCTG	21598
QY	20460	CCCACCTCAGCCTCCCAAGCACTGGGATTTACAGGCAATGAGCCACCGTCCAGCCTGTT	20519				

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 Db 94588 TGTGCTGATAAAGATATACCTCAGACTGATATATTAAGAAAGAGAGGTTTAATGG 94647
 QY 26038 ACTCAGAGTTCCAGTGGCTGAGGAAGCTTCAATCATGTTGGAAGCAAGAGCATGT 26097
 Db 94648 ACTCAGAGTTCCAGTGGCTGAGGAAGCTTCAATCATGTTGGAAGCAAGAGCATGT 94707
 QY 26098 CTTACATGCGAGCAGACAGAGAGATAGAACCRAGGATTTCCCTTATTAACACCATC 26157
 Db 94708 CTTACATGCGAGCAGACAGAGAGATAGAACCRAGGATTTCCCTTATTAACACCATC 94767
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 Db 94768 AGATCTTGTGAGACTTATTCACCTACCAACAGAACATATGGGTAAACCGCCCTCATGAT 94827
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 Db 94948 ATTTCTTCCCATCTTTATTCCTCAACCGGTACAACAGACCTCTTTTTTTTTTTTT 95007
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QY	28133	AAAGGCAATTTCTTAGGAGAGTTCTTCTCTGTAGAGTCTTAAGGGTTCCATGGAATCC	28132	Db	97828	AGGTAGGATAATCACTTGAACCCGGAAGACAGAGGTGCGAGTGCAGATTGTGCCAC	97887
Db	96748	AAAGAGCAATTTCTTAGGAGAGTTCTTCTCTGTAGAGTCTTAAGGGTTCCATGGAATCC	96807	QY	29266	TGCACCTCAGCGGGGCAACAGAGTGCAGCGGTCTCAAAAAATTTTAAAAAATTTAAAAA	29325
QY	28193	TTAAAAAGCATCAGAGTATGTGAGTGCATATGGGAGGAAGCATTTTAGCCAGAGCATTTGTCC	28252	Db	97888	TGCACTCCAGCGGGGCAACAGAGTGCAGCGGTCTCAAAAAATTTTAAAAAATTTAAAAA	97947
Db	96808	TTAAAAAGCATCAGAGTATGTGAGTGCATATGGGAGGAAGCATTTTAGCCAGAGCATTTGTCC	96867	QY	29326	TAATAGAGCAAGAAAGACCAAGTTATTTCAGGAGGATCCACCCCAATGACTCAAAATAC	29385
QY	28253	TCCCATGTGATATTAATTTTAAAAACAAAGCTATAAAAAAAGTTGAAAATCTACTAGC	28312	Db	97948	TAATAGAGCAAGAAAGACCAAGTTATTTCAGGAGGATCCACCCCAATGACTCAAAATAC	98007
Db	96868	TCCCATGTGATATTAATTTTAAAAACAAAGCTATAAAAAAAGTTGAAAATCTACTAGC	96927	QY	29386	CTCCACCAAGGCTTCACTTCCACACTGGGATCAATTTCCGTATGAGATTGGAGGAGA	29445
QY	28313	TTAGCATCAGCCTGACATTTAATGGGCTCGTAATCAAAACCTTAATTTGACTTTTAGCCA	28372	Db	98008	CTCCACCAAGGCTTCACTTCCACACTGGGATCAATTTCCGTATGAGATTGGAGGAGA	98067
Db	96928	TTAGCATCAGCCTGACATTTAATGGGCTCGTAATCAAAACCTTAATTTGACTTTTAGCCA	96987	QY	29446	CAATATCCAAACTATATACATATAGTAAATGAACATAGTACCTTATCTATAGAAAGCAATG	29505
QY	28373	GTATGCTACTAGCCAACTACAGACAACACATTTTAAACCAATTTAGACTAATAGTTGT	28432	Db	98068	CAATATCCAAACTATATACATATAGTAAATGAACATAGTACCTTATCTATAGAAAGCAATG	98127
Db	96988	GTATGCTACTAGCCAACTACAGACAACACATTTTAAACCAATTTAGACTAATAGTTGT	97047	QY	29506	GCTAGACAACCTGTTGAATGGCTAACCAACTCTGTTTCTTATGCTCTAGAGGGG	29565
QY	28433	CATCAGTGGAAATCAAGTTTGGCAATCTTCCATGCTTTCCTACACCAATACCTTTTCT	28492	Db	98128	GCTAGACAACCTGTTGAATGGCTAACCAACTCTGTTTCTTATGCTCTAGAGGGG	98187
Db	97048	CATCAGTGGAAATCAAGTTTGGCAATCTTCCATGCTTTCCTACACCAATACCTTTTCT	97107	QY	29566	GTGATGATGAGTTTCTGTCAAAAGGAGAAAAAATGTATAGTCAGTTTGTGTGTG	29625
QY	28493	GGAAATGCTGCTACTCATCTTCTGTGTTGAATCTATACCCAACTTTAAAAACCTAGCT	28552	Db	98188	GTGATGATGAGTTTCTGTCAAAAGGAGAAAAAATGTATAGTCAGTTTGTGTGTG	98247
Db	97108	GGAAATGCTGCTACTCATCTTCTGTGTTGAATCTATACCCAACTTTAAAAACCTAGCT	97167	QY	29626	TGTTGTCATGTAAAGAGATCAAGAGAGAAAGAAACAGAGAAATCATGAAGAGGAGGGA	29685
QY	28553	CAAGTTTCAACACTTCCATTCATTTCAAAAGAGCTTTCCTTCTTAAAGATTAAAGA	28612	Db	98248	TGTTGTCATGTAAAGAGATCAAGAGAGAAAGAAACAGAGAAATCATGAAGAGGAGGGA	98307
Db	97168	CAAGTTTCAACACTTCCATTCATTTCAAAAGAGCTTTCCTTCTTAAAGATTAAAGA	97227	QY	29686	ATATAAGAAATATACATAGAAAAAGCAAAATATCTTTTATCAGTAATACCCAAAGGG	29745
QY	28613	ACTCATTTTCATGAATCTTTTGGCAATTTATTGCACACATGCTTGTGTGTATTTGT	28672	Db	98308	ATATAAGAAATATACATAGAAAAAGCAAAATATCTTTTATCAGTAATACCCAAAGGG	98367
Db	97228	ACTCATTTTCATGAATCTTTTGGCAATTTATTGCACACATGCTTGTGTGTATTTGT	97287	QY	29746	GTAGAAATGTAGTAATATCTTCTTCTTCTGCTGTAGTTCACCTTTTGTGACCTT	29805
QY	28673	GTTCA-GCCTCATATGCCCAAGGTGTTTGTAGACTTCTTAAGCGCAAAATGATGCTCT	28731	Db	98368	GTAGAAATGTAGTAATATCTTCTTCTTCTGCTGTAGTTCACCTTTTGTGACCTT	98427
Db	97288	GTTTCATGCTCATATGCCCAAGGTGTTTGTAGACTTCTTAAGCGCAAAATGATGCTCT	97347	QY	29806	TATTTGATGAATTCACATCGAAGACATTAACCTTAAGGCTTCCCAATATTTTGGAGA	29865
QY	28732	AAACACTTTCATCTTTCATAGTGTCTTAGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTT	28791	Db	98428	TATTTGATGAATTCACATCGAAGACATTAACCTTAAGGCTTCCCAATATTTTGGAGA	98487
Db	97348	AAACACTTTCATCTTTCATAGTGTCTTAGTGTCTTAGTGTCTTAGTGTCTTAGTGTCT	97407	QY	29866	TAAAGAGGCTGTATGCTCTTTTATAGATGAAACCTTGGGTCAATTAATCAACAA	29925
QY	28792	GAGGCTGGGAAATTTTAAAAAGAGGTTTATTTGGTCTACAGTCTTGCA-GCTATAT	28850	Db	98488	TAAAGAGGCTGTATGCTCTTTTATAGATGAAACCTTGGGTCAATTAATCAACAA	98547
Db	97408	GAGGCTGGGAAATTTTAAAAAGAGGTTTATTTGGTCTACAGTCTTGCAAGGCTATAT	97467	QY	29926	GGACATACAAAGAAATGGAGCATAACTGCCAGTCTCTGACTGTAGATTGGATTCCCA	29985
QY	28851	AAGAAGCATAGTGTACGATCTGCTTCAGGTGAGGCTTTCAGGAGTTTCCACCCATGCT	28910	Db	98548	GGACATACAAAGAAATGGAGCATAACTGCCAGTCTCTGACTGTAGATTGGATTCCCA	98607
Db	97468	AAGAAGCATAGTGTACGATCTGCTTCAGGTGAGGCTTTCAGGAGTTTCCACCCATGCT	97527	QY	29986	GTGCTGTCTTGTCCACCTTTGTTTACTCTTCTTAAAGTTATGATCTTTTCTGTGCATAG	30045
QY	28911	AGAAGGCAAGGGGAGCAGGCATCACATATCAAGAGAGGAGGAAAAAAGGAAGAA	28970	Db	98608	GTGCTGTCTTGTCCACCTTTGTTTACTCTTCTTAAAGTTATGATCTTTTCTGTGCATAG	98667
Db	97528	AGAAGGCAAGGGGAGCAGGCATCACATATCAAGAGAGGAGGAAAAAAGGAAGAA	97587	QY	30046	GAAATTCATAGTATTTCCCATCACCTTGGGATATCATAGCTTCAAGTTCAGTCCCTC	30105
QY	28971	AGGAGGCTGCCATTTCTTCAACATCAGTTCTTGTGGAACTAATGGGCAAGAGGCT	29030	Db	98668	GAAATTCATAGTATTTCCCATCACCTTGGGATATCATAGCTTCAAGTTCAGTCCCTC	98727
Db	97588	AGGAGGCTGCCATTTCTTCAACATCAGTTCTTGTGGAACTAATGGGCAAGAGGCT	97647	QY	30106	TATGACTCTAATAACATCAACAGTAAGTTTCTTCGAGCACTTACTGAGTATATCAT	30165
QY	29031	GGGACGGTGGCTCATGCTGTAATCCAGCCCTTTGGGAGACCAGGTTGGGTGATCAC	29090	Db	98728	TATGACTCTAATAACATCAACAGTAAGTTTCTTCGAGCACTTACTGAGTATATCAT	98787
Db	97648	GGGACGGTGGCTCATGCTGTAATCCAGCCCTTTGGGAGACCAGGTTGGGTGATCAC	97707	QY	30166	GTGTTCTCAGCAGACCCACAGATCTCAACAGAACTTAGCTGAAGCTGTAGAAATGAA	30225
QY	29091	CTGAAGTCAGAGCCCTGAGACAGCAGCTGGCAATGTGGTGAACCTCCGCTCTCTATAAA	29150	Db	98788	GTGTTCTCAGCAGACCCACAGATCTCAACAGAACTTAGCTGAAGCTGTAGAAATGAA	98847
Db	97708	CTGAAGTCAGAGCCCTGAGACAGCAGCTGGCAATGTGGTGAACCTCCGCTCTCTATAAA	97767	QY	30226	TAGTAAAGTACTGCTGCTGCAATCTGAGTACTCAAGCGATGCAAAATGATTCCTTTAAT	30285
QY	29151	ATCAAAAAATTAGCTGGCTGTGGCTGTACTGTAGTCCAGATACTCAGGAGGCTG	29210	Db	98848	TAGTAAAGTACTGCTGCTGCAATCTGAGTACTCAAGCGATGCAAAATGATTCCTTTAAT	98907
Db	97768	ATCAAAAAATTAGCTGGCTGTGGCTGTACTGTAGTCCAGATACTCAGGAGGCTG	97827	QY	30286	GTAATTTGAGGCTTGTGAGTTTGTCTCATGAGAGAGTGCTACTGCATCCATGTTATA	30345
QY	29211	AGGTAGGATAATCACTTGAAACCCGGAAGACAGAGGTTGCGAGTCAGC-----TTGTGCCAC	29265				

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Db 105442 CCAATATTTATCACTATTTCCCTTAGGGAACCTTAGATCTGTGATATTTGAAATATAA 105501

QY	36878	AGCCTCTCCATTTGGCCCTTTAAAAAGGTTTGTGGTAAACACACACCATTAACATTCACAGT	36937	Db	106579	GTCAGTACGTGTGGGCAATTTGCTAGCACAGGACCAAAAGATTAAGACATTTGTAGC	106638
Db	105502	AGCCTCTCCATTTGGCCCTTTAAAAAGGTTTGTGGTAAACACACACCATTAACATTCACAGT	105561	QY	38017	TTTCCTTAAGTTGCTCACTGAGTAATAAGAGAGACAGAAAGGTAAACAGGTAAGTGCAAA	38076
QY	36938	TCCTTATTTATGAGGCGCTGATTCGACATTAATTCATATTTCTCATGTTTCTCCGATGAG	36997	Db	106639	TTTCCTTAAGTTGCTCACTGAGTAATAAGAGAGACAGAAAGGTAAACAGGTAAGTGCAAA	106698
Db	105562	TCCTTATTTATGAGGCGCTGATTCGACATTAATTCATATTTCTCATGTTTCTCCGATGAG	105621	QY	38077	AATACATCAATTCAGCAATAGTGTTCATAGTGGCTATGGAGAGACGCTCACAACCTTT	38136
QY	36998	GAATTCACATAATAGTGTGTTGAAGGCTAAAGACTTCAAAGCAGATTCTTTACTATTTTAA	37057	Db	106699	AATACATCAATTCAGCAATAGTGTTCATAGTGGCTATGGAGAGACGCTCACAACCTTT	106758
Db	105622	GAATTCACATAATAGTGTGTTGAAGGCTAAAGACTTCAAAGCAGATTCTTTACTATTTTAA	105681	QY	38137	GTTTAAACAGATTGTTCTTTCAAGGATTTGCATATGATTTGATTTGAAAGCATATGATACA	38196
QY	37058	TCATTGAAAAATATTCATATTTGTTGTAATTAAGTGAAGTCTTCCTAGAGAAAAATGACAA	37117	Db	106759	GTTTAAACAGATTGTTCTTTCAAGGATTTGCATATGATTTGATTTGAAAGCATATGATACA	106818
Db	105682	TCATTGAAAAATATTCATATTTGTTGTAATTAAGTGAAGTCTTCCTAGAGAAAAATGACAA	105741	QY	38197	TTTTTTGCAATTAACACACAGGAATACATAAATAAAATGCATCAGTATTTTTTACAATAAG	38256
QY	37118	CTCAATAATCTTAAATGTAACCTCCAAAGAAAAAGGCTGCARAGTGACATTTAGTATATAG	37177	Db	106819	TTTTTTGCAATTAACACACAGGAATACATAAATAAAATGCATCAGTATTTTTTACAATAAG	106878
Db	105742	CTCAATAATCTTAAATGTAACCTCCAAAGAAAAAGGCTGCARAGTGACATTTAGTATATAG	105801	QY	38257	CTACTAAGAGCTACTAGAAAAACCTGGGAATTTCTTAAACCTTTACCATGCTACTTGTCTTA	38316
QY	37178	AGTCACATTTCTTAAGGCGCTTGTCTCTCTCTCTGA - TTCTTATCATCTTTGAAGGTTAT	37236	Db	106879	CTACTAAGAGCTACTAGAAAAACCTGGGAATTTCTTAAACCTTTACCATGCTACTTGTCTTA	106938
Db	105802	AGTCACATTTCTTAAGGCGCTTGTCTCTCTCTCTGA - TTCTTATCATCTTTGAAGGTTAT	105861	QY	38317	AAATATTTATTTTATGTTATTTTGTACATTTCTTTACCTACACAAACACCACTGTTTTTC	38376
QY	37237	GTCAAGGCTGAGCTTCAAAATCAATTTTAAATTTATATGGCCTTCTTTAAATGTGAGTT	37296	Db	106939	AAATATTTATTTTATGTTATTTTGTACATTTCTTTACCTACACAAACACCACTGTTTTTC	106998
Db	105862	GTCAAT - GGCTGACTTCAAAATC - ACTTTTAAATTTATATGGCCTTCTTTAAATGTGAGTT	105919	QY	38377	TTCAATTTCTTAGTCTTATTTTAAACCTTCACACCTTTTACCATGCTACTTATTTACTACC	38436
QY	37297	CTGAAGGTGAGGCGCTTATCTTTCTTTGCTCCAGATTTTTTTTACCGGCTCATTAACCA	37356	Db	106999	TTCAATTTCTTAGTCTTATTTTAAACCTTCACACCTTTTACCATGCTACTTATTTACTACC	107058
Db	105920	CTGAAGGTGAGGCGCTTATCTTTCTTTGCTCCAGATTTTTTTTACCGGCTCATTAACCA	37356	QY	38437	ATCTGTTAGTTCTCTCTGCTCTGAATGAACAAAAATGGCAGAAATGTAACACGAGGCGAA	38496
QY	37357	AGCATCTTAAACAAACCTTAAACAAATAATTTTAAAGGTTTAAACGAGTCTTTTATACC	37416	Db	107059	ATCTGTTAGTTCTCTCTGCTCTGAATGAACAAAAATGGCAGAAATGTAACACGAGGCGAA	107118
Db	105980	AGCATCTTAAACAAACCTTAAACAAATAATTTTAAAGGTTTAAACGAGTCTTTTATACC	106039	QY	38497	CAGATTTTGAAGAGAGTATTCAGAGGTAGAGAAATAGTCAAGACACATATGATATAA	38556
QY	37417	TAAACATCCUATTTTATCTTTCCCTTTTGACATTAAGGTTTAAACGAGTCTTTTATACC	37476	Db	107119	CAGATTTTGAAGAGAGTATTCAGAGGTAGAGAAATAGTCAAGACACATATGATATAA	107178
Db	106040	TAAACATCCUATTTTATCTTTCCCTTTTGACATTAAGGTTTAAACGAGTCTTTTATACC	106098	QY	38557	CGAAAAAATAATTAACCTTTATACATAACACTTATAGACACATTTAAAAAGTTTAAAGATC	38616
QY	37477	CTCTGCTCCATTTTCTCATCTGCTAACTATATGCAAGATTAACCACTGCTTTTCAAC	37536	Db	107179	CGAAAAAATAATTAACCTTTATACATAACACTTATAGACACATTTAAAAAGTTTAAAGATC	107238
Db	106099	CTCTGCTCCATTTTCTCATCTGCTAACTATATGCAAGATTAACCACTGCTTTTCAAC	106158	QY	38617	TCAGAGCTATGCTGTAATAGATAGGAGTAAAACTCTATTAAGTAATTAAGAAAAATAAC	38676
QY	37537	ATAATTTGGCCAACTACAGAAAGTTTCAAGTCTCTTTTAAATGACCACTCTGCT	37596	Db	107239	TCAGAGCTATGCTGTAATAGATAGGAGTAAAACTCTATTAAGTAATTAAGAAAAATAAC	107298
Db	106159	ATAATTTGGCCAACTACAGAAAGTTTCAAGTCTCTTTTAAATGACCACTCTGCT	106218	QY	38677	AAGAACAGTGAATTTCTTAATGAATGCATGAATCAAAACTGTAATCTATCGTCTAATTC	38736
QY	37597	ACCTCCCACTTTGACATCTTCTCTCTCACTTGGCACCTTACCCAGTGTTCAGATTC	37656	Db	107299	AAGAACAGTGAATTTCTTAATGAATGCATGAATCAAAACTGTAATCTATCGTCTAATTC	107358
Db	106219	ACCTCCCACTTTGACATCTTCTCTCTCACTTGGCACCTTACCCAGTGTTCAGATTC	106278	QY	38737	ATAATCTTGAATGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT	38796
QY	37657	CTCCTTTAGGATGCTTTCAGAGCAGCTACACAGTTGGTACTATATTTATATCATCCTTGT	37716	Db	107359	ATAATCTTGAATGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT	107418
Db	106279	CTCCTTTAGGATGCTTTCAGAGCAGCTACACAGTTGGTACTATATTTATATCATCCTTGT	106338	QY	38797	CTCTGTACCCAGCTAGAGTACAGTGGCGTGATCTCAGCTCACTGCAACTCCACCTCC	38856
QY	37717	ACACAGGCTTGTGGGATTAATGAATGGAGAGAGGAGAACTGGAAGTAGTTCAGGCCA	37776	Db	107419	CTCTGTACCCAGCTAGAGTACAGTGGCGTGATCTCAGCTCACTGCAACTCCACCTCC	107478
Db	106339	ACACAGGCTTGTGGGATTAATGAATGGAGAGAGGAGAACTGGAAGTAGTTCAGGCCA	106398	QY	38857	CAGTTTCAAGCGATTCCTGCTGCTCAGCTCCTGAGTAGTGGGATTTACAGAGCCCTGCC	38916
QY	37777	GAGCTAGGAAATTAACCACTCCAGGTCTCAGTCTGCAAGGGAGCTCAGCTTAA	37836	Db	107479	CAGTTTCAAGCGATTCCTGCTGCTCAGCTCCTGAGTAGTGGGATTTACAGAGCCCTGCC	107538
Db	106399	GAGCTAGGAAATTAACCACTCCAGGTCTCAGTCTGCAAGGGAGCTCAGCTTAA	106458	QY	38917	ACTGCACCCGCTAAATTTCTGTAATTTTATAGATAGAGTGGGTTTACCATCTTTGGCCAGG	38976
QY	37837	CACATGGAGTCTAGAAACTTGTGCTGGACCTTGACCAACACAGCCCATGGAGTCCATA	37896	Db	107539	ACTGCACCCGCTAAATTTCTGTAATTTTATAGATAGAGTGGGTTTACCATCTTTGGCCAGG	107598
Db	106459	CACATGGAGTCTAGAAACTTGTGCTGGACCTTGACCAACACAGCCCATGGAGTCCATA	106518	QY	38977	CTGTCTTGAACCTCTGACCTCATGATCCACAGCCTTGGCCCTCCCAAGTGTGGGATT	39036
QY	37897	CAGTGTCAATAGGATTTCCAGGAAATTTGCTATATTTTATTAAGAGAACTTACCAAGT	37956	Db	107599	CTGTCTTGAACCTCTGACCTCATGATCCACAGCCTTGGCCCTCCCAAGTGTGGGATT	107658
Db	106519	CAGTGTCAATAGGATTTCCAGGAAATTTGCTATATTTTATTAAGAGAACTTACCAAGT	106578	QY	39037	ACAGGCTGAGCCACACAGCCTCTGTCGAATGCTTTATTTATTTTGAAGAGACCAATGGGC	39096
QY	37957	GTCAGTACGCTGTGGGCAATTTGCTAGGCACAGGACCAAAAGATTAAGACATTTGTAGC	38016				

repeat_region	complement(32130..32248)	Db	121	CTGGGCTCTGATGATATTAATCTGATATCTCAACCTTTTGTTCGAGTGTAGGC	180
repeat_region	/rpt_family="MLT1"	QY	563	CATTACATTTAGTCTAATATAGACATGGTTGCTATACCACTTTTTCATTTGT	622
repeat_region	/rpt_family="Alu"	Db	181	CATTACATTTAGTCTAATATAGACATGGTTGCTATACCACTTTTTCATTTGT	240
repeat_region	complement(34169..34233)	QY	623	TTTATATGTAGGCCATCTTTTCATTTGTTCTTTTTCATCTTTGACCATTTTCTTTAGTAC	682
repeat_region	/rpt_family="MIR"	Db	241	TTTATATGTAGGCCATCTTTTCATTTGTTCTTTTTCATCTTTGACCATTTTCTTTAGTAC	300
repeat_region	/rpt_family="Alu"	QY	683	TGATACATTTTCTTTTGTATTTTCAATATATCTATTTGGCTTTTATAGTATACCTCTTAAATTT	742
repeat_region	/rpt_family="MIR"	Db	301	TGATACATTTTCTTTTGTATTTTCAATATATCTATTTGGCTTTTATAGTATACCTCTTAAATTT	360
repeat_region	complement(35993..36081)	QY	743	TTTTTTTCTGTTTATGTAGGATTTTAAATATATCATCTTTTAACTTATCAGATACCTT	802
repeat_region	/rpt_family="MIR"	Db	361	TTTTTTTCTGTTTATGTAGGATTTTAAATATATCATCTTTTAACTTATCAGATACCTT	420
repeat_region	/rpt_family="Alu"	QY	803	CAATATAGTATTTTACCAGCTCAAGTGTAAATGTAGAAACCTTTACAAAGATATATTTTCATT	862
repeat_region	complement(42817..42877)	Db	421	CAATATAGTATTTTACCAGCTCAAGTGTAAATGTAGAAACCTTTACAAAGATATATTTTCATT	480
repeat_region	/rpt_family="MIR"	QY	863	TCTGTCTCTAAATTTTATATGCTA-TGCTATATAATACATTTAGTTTGTGTTGTTT	921
repeat_region	/rpt_family="Alu"	Db	481	TCTGTCTCTAAATTTTATGCTATTTGCTATATAATACATTTAGTTTGTGTTGTTT	540
repeat_region	complement(46257..46490)	QY	922	TACCTTATTTGCTGTTGGCTGGGTCAGCAAAACATTTTCTGFAAAGGGCTAGATAGTACAG	981
repeat_region	/rpt_family="L1"	Db	541	TACCTTATTTGCTGTTGGCTGGGTCAGCAAAACATTTTCTGFAAAGGGCTAGATAGTACAG	600
repeat_region	/rpt_family="Alu"	QY	982	GCATACCTTGAGATATCTGTTGGGTTTGGTTCATACCAACCAATATACAAATATGCAA	1041
repeat_region	complement(50349..50611)	Db	601	GCATACCTTGAGATATCTGTTGGGTTTGGTTCATACCAACCAATATACAAATATGCAA	660
repeat_region	/rpt_family="L1"	QY	1042	GAAGTGGATATCAACAATAAAGTGAGTCACCAAGCTCTTTTGGCTTCCAGTGCATATAAA	1101
repeat_region	/rpt_family="Alu"	Db	661	GAAGTGGATATCAACAATAAAGTGAGTCACCAAGCTCTTTTGGCTTCCAGTGCATATAAA	720
repeat_region	complement(51085..51374)	QY	1102	AGTTTGGCTTATACACATCTGTTAGTGTGCAATAGTGTATGCTTAAATAAAA	1161
repeat_region	/rpt_family="L1"	Db	721	AGTTTGGCTTATACACATCTGTTAGTGTGCAATAGTGTATGCTTAAATAAAA	780
repeat_region	complement(60338..60470)	QY	1162	CACATACCTTAATTTTAAATGCTTTTATTAATAAATAAATGCTTAAATAAATGCTTAAATAA	1221
repeat_region	/rpt_family="MIR"	Db	781	CACATACCTTAATTTTAAATGCTTTTATTAATAAATAAATGCTTAAATAAATGCTTAAATAA	840
repeat_region	complement(61353..61521)	QY	1222	CAGTGAGTTGTAATCTTTTGGTGGTGAAGTCTTTTCTTATTTATGATGATCGGGGG	1281
repeat_region	/rpt_family="Alu"	Db	841	CAGTGAGTTGTAATCTTTTGGTGGTGAAGTCTTTTCTTATTTATGATGATCGGGGG	900
repeat_region	/rpt_family="MIR"	QY	1282	TCAGTGCTGAAGCTTAGGTTAGGTTGGCTGTGGAGTTTCTTAAACCAACAGTGAAGATTGCAA	1341
repeat_region	/rpt_family="MIR"	Db	901	TCAGTGCTGAAGCTTAGGTTAGGTTGGCTGTGGAGTTTCTTAAACCAACAGTGAAGATTGCAA	960
repeat_region	complement(65459..65548)	QY	1342	TATCAGTTGACTCTTCTTCTCATGAAAGATTCTCTCTAGTGTGATGCTTTTGTATAG	1401
repeat_region	/rpt_family="MER5"	Db	961	TATCAGTTGACTCTTCTTCTCATGAAAGATTCTCTCTAGTGTGATGCTTTTGTATAG	1020
repeat_region	/rpt_family="MER20"	QY	1402	CATTTTATGACAGTACAACTTTTCTTGAATAATTTCTGATCCATTTGTCATTTTCAACAATTTT	1460
repeat_region	complement(67562..68084)	Db	1021	CATTTTATGACAGTACAACTTTTCTTGAATAATTTCTGATCCATTTGTCATTTTCAACAATTTT	1080
repeat_region	/rpt_family="MER41"	QY	1461	GCITTTACACCTTAAGTTATATAATTTCTGATCCATTTGTCATTTTCAACAATTTT	1520
repeat_region	complement(75521..75548)	Db	1081	GCITTTACACCTTAAGTTATATAATTTCTGATCCATTTGTCATTTTCAACAATTTT	1140
repeat_region	/rpt_family="MIR"	QY	1521	CACAGTGTCTTACCAGGAGTAGATCTCTCATTTCTTCCAGATGGAATCTTTTGTCTCAT	1580
repeat_region	/rpt_family="MIR"	Db	1141	CACAGTGTCTTACCAGGAGTAGATCTCTCATTTCTTCCAGATGGAATCTTTTGTCTCAT	1200
repeat_region	complement(75521..75548)	QY	1581	CCATAGAGAAATTTCTCTCATCTGTTTCAAGTTTATCATGAGATTGCGAATACAGTCA	1640

ORIGIN

Query Match 97.2%; Score 38866.2; DB 9; Length 69058;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 39507; Conservative 0; Mismatches 93; Indels 85; Gaps 50;

QY	383	CCACTCTGGCTTTTAAAATTTAGTATTTTATGGTATATATTTTCCCTTTTATTTT	442
Db	1	CCACTCTGGCTTTTAAAATTTAGTATTTTATGGTATATATTTTCCCTTTTATTTT	60
QY	443	TAAGTTTATAGTATTTTCTTATACCTTAAAGTGGTGCTTTATAGGAGCATATAT	502
Db	61	TAAGTTTATAGTATTTTCTTATACCTTAAAGTGGTGCTTTATAGGAGCATATAT	120
QY	503	CTGGGCTCTGATGATATTAATCTGATAAATCTCAACCTTTTGTGGAGTGTAGGC	562

Db CCATAAGAGAAATTCCTCATCTGTTCAAGTTTATCATAGATTGCGCAATACAGTCA 1260
QY TGFCTTCAGGCTCCTCCTCACTTTTAAATCCAGTCTCTTGCTGTTTCTTACCACTCTGT 1700
Db TGFCTTCAGGCTCCTCCTCACTTTTAAATCCAGTCTCTTGCTGTTTCTTACCACTCTGT 1320
QY GFTTCCTTCCTCATGTAAGTCTTGAACTCTCCAAAGTCATCCATGAGGTTGGAATCGA 1760
Db GFTTCCTTCCTCATGTAAGTCTTGAACTCTCCAAAGTCATCCATGAGGTTGGAATCGA 1380
QY CTTCCTTCCTCATGTAAGTCTTGAACTCTCCAAAGTCATCCATGAGGTTGGAATCGA 1820
Db CTTCCTTCCTCATGTAAGTCTTGAACTCTCCAAAGTCATCCATGAGGTTGGAATCGA 1440
QY AATGGCACCTGGAATGGAATCTTCCAAAGGTTTCAATTTACTTAGTCCAGATCC 1880
Db AATGGCACCTGGAATGGAATCTTCCAAAGGTTTCAATTTACTTAGTCCAGATCC 1500
QY ATCCATCCAGAGATCCACTTTCAATGCCAGTTATAGCCTTATGGAATGTAATTTCTTCAA 1940
Db ATCCATCCAGAGATCCACTTTCAATGCCAGTTATAGCCTTATGGAATGTAATTTCTTCAA 1560
QY TAATAAGGCTTGAAGTTGAAATTTACTCTCTTGATCCATTTCTGCAAAATAGATGTTGTG 2000
Db TAATAAGGCTTGAAGTTGAAATTTACTCTCTTGATCCATTTCTGCAAAATAGATGTTGTG 1620
QY TTAGCAGGATGAAAGCAATTAATCTTTTGTATCATGTCATCAGAGCTCTTGCTGGA 2060
Db TTAGCAGGATGAAAGCAATTAATCTTTTGTATCATGTCATCAGAGCTCTTGCTGGA 1680
QY CCAGGTATATGTCAGTGAGCAATTAATCTTTGAAAGGAAATTTCTTACAGCTAGG 2120
Db CCAGGTATATGTCAGTGAGCAATTAATCTTTGAAAGGAAATTTCTTACAGCTAGG 1740
QY TCTCAACAAATGGGCTTAAATATTTGGTCCACCATTTCTGTAACTGATGTCGTCACT 2180
Db TCTCAACAAATGGGCTTAAATATTTGGTCCACCATTTCTGTAACTGATGTCGTCACT 1800
QY AAATTTGATGTTTCAATTTATAGACAGCAGGAGATGATGATGATGATGATGATGATG 2240
Db AAATTTGATGTTTCAATTTATAGACAGCAGGAGATGATGATGATGATGATGATGATG 1860
QY AACTTTGATGTTTCAATTTATAGACAGCAGGAGATGATGATGATGATGATGATGATG 2300
Db AACTTTGATGTTTCAATTTATAGACAGCAGGAGATGATGATGATGATGATGATGATG 1920
QY AGCCCCCAACAGAGAGTCACTTATTTTGAAGCTTTGAGCCCAAGGCTCGACTTCTC 2360
Db AGCCCCCAACAGAGAGTCACTTATTTTGAAGCTTTTGAAGCTTTGAGCCCAAGGCTCGACTTCTC 1980
QY CTCCTCGTTTACAAAAGTCTTAAATGGCATCTTCTTCCAAATATAAGGCTGTTTATCTAC 2420
Db CTCCTCGTTTACAAAAGTCTTAAATGGCATCTTCTTCCAAATATAAGGCTGTTTATCTAC 2040
QY ATTGAAATCTGTTTGTAGTACGACCTTCAATCAATGATATCTATCTAGTCTCTTGG 2480
Db ATTGAAATCTGTTTGTAGTACGACCTTCAATCAATGATATCTATCTAGTCTCTTGG 2100
QY ATAACTTGTGAGCTTCTACATCAGCATTTGCTTACTTCACTTGTACTCTTATGTAATGG 2540
Db ATAACTTGTGAGCTTCTACATCAGCATTTGCTTACTTCACTTGTACTCTTATGTAATGG 2160
QY AGTGGCATTTCTCTGATGATGAAACCAACCTCTGTAGCTTCCAACTTTCTTCTG 2600
Db AGTGGCATTTCTCTGATGATGAAACCAACCTCTGTAGCTTCCAACTTTCTTCTG 2220
QY TAGTTTCTGCTCTCTCAGCTTTCATAGACTTTGAGAGTATTAGAGCTTCTGTTGA 2660
Db TAGTTTCTGCTCTCTCAGCTTTCATAGACTTTGAGAGTATTAGAGCTTCTGTTGA 2280
QY TTAGATTTGGCTTCAGGAAATGTTGTGGTGGTTGATCTTCTATCCAGACCACTTAAA 2720
Db TTAGATTTGGCTTCAGGAAATGTTGTGGTGGTTGATCTTCTATCCAGACCACTTAAA 2340

QY CTTTATCCATATCAGCAATAAGGCTGTTTGTCTTCTTATTTTGTGTTGTTTCACTGGAG 2720
Db CTTTATCCATATCAGCAATAAGGCTGTTTGTCTTCTTATTTTGTGTTGTTTCACTGGAG 2400
QY TAGCACTTTTAAATTTGCTTCAAGATATTTCTTTGCATTCACAACTTGGCTGACTGGTG 2840
Db TAGCACTTTTAAATTTGCTTCAAGATATTTCTTTGCATTCACAACTTGGCTGACTGGTG 2460
QY CAAGAGCCCTAGCTTTTCAAGCTATCTTTGACATGCTTCTCTCACTAAGCTTAAAT 2900
Db CAAGAGCCCTAGCTTTTCAAGCTATCTTTGACATGCTTCTCTCACTAAGCTTAAAT 2520
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Db GCATATGCCCTGTAATTTCCAAACACATTAAGAGGCCAAGGTGGGAGGATGCTTGAACCCAG 2640
QY GAGGTGGAGGTTGTAGAGATCACCACCTGCTTCCGTCTCTGATCAGAGCAAGA-CC 3079
Db GAGGTGGAGGTTGTAGAGATCACCACCTGCTTCCGTCTCTGATCAGAGCAAGA-CC 2700
QY TTTTCTCAAAATAAAATGAGAGGTTGCTTCTTTTGTGAGCCCATAGAGCCATA 3139
Db TTTTCTCAAAATAAAATGAGAGGTTGCTTCTTTTGTGAGCCCATAGAGCCATA 2760
QY GTATGATTTTAAATTTGSCCTAAATTTCAATACTGTTGCTCTCAGAGAAATAGGAGGCTG 3199
Db GTATGATTTTAAATTTGSCCTAAATTTCAATACTGTTGCTCTCAGAGAAATAGGAGGCTG 2820
QY AAGAGAGGAGAGAGGTTGGGGAATGGCTGCTCAGTGGAGCAGTCAGAACACACATAACA 3259
Db AAGAGAGGAGAGAGGTTGGGGAATGGCTGCTCAGTGGAGCAGTCAGAACACACATAACA 2880
QY CTAATAAATTTGTTGCTGCTTATATGATGTTGTTGATGCTGCTGCTGCTGCTGCTGCTG 3319
Db CTAATAAATTTGTTGCTGCTTATATGATGTTGTTGATGCTGCTGCTGCTGCTGCTGCTG 2940
QY TAGTTACAGCAAAATATCAGTATCAGATCACCATAACAGATATAAGAAATCATGSCAAA 3379
Db TAGTTACAGCAAAATATCAGTATCAGATCACCATAACAGATATAAGAAATCATGSCAAA 3000
QY GTTTGAAATATTTCTTGAAATTTAGCAAAATGAGCAAGTGGCAATAGAAATAGAAATATG 3439
Db GTTTGAAATATTTCTTGAAATTTAGCAAAATGAGCAAGTGGCAATAGAAATAGAAATATG 3059
QY CTTTGGAAAAAATTTGCTGATAGCTTGTCTCATCGCAAGTTTGGCATACGCTTCAA 3499
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Db TTTTAAAAAACAACAAATATCTAGGAAGTTCAATAAAGTGAAGTGAATAGAAATAGAAAT 3178
QY CCTGTAAATATTTTCAAGCTTTCCAGACCATAGGTTTCTGTTGCAACTGCTCACTCTG 3619
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QY CTTTGAATATTTTCAAGCTTTCCAGACCATAGGTTTCTGTTGCAACTGCTCACTCTG 3679
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QY CTTTGGAGCCCAAGGTTGGATCTCTTACTTAAATAATGAGGCTGTAAATCCCAACA 3799
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QY ACATGGCAAAACCCCGTCTCTTACTTAAATAATGAGGCTGTAAATCCCAACA 3799
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QY 3800 TAGTCCAGCTACTTGGAGGCTGAGCGAGGAGAAATCTCTGTGAACCCGGGAAGGGAGGT 3859
Db TAGTCCAGCTACTTGGAGGCTGAGCGAGGAGAAATCTCTGTGAACCCGGGAAGGGAGGT 3478
QY 3860 TACAGTGAAGCAAGATTGTGCCACTGCACTCCAGCCTGGGCAACAGAGTGAGACTGTCTC 3919
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QY 3920 AAAAAAAGAAAGAAAGAAATACACATAAATGAATGTATGGCTGTGTACCAAG 3979
Db AAAAAAAGAAAGAAAGAAATACACATAAATGAATGTATGGCTGTGTACCAAG 3598
QY 3980 TATATCCTCATGCTCTAGCTGTGCAACCCCTGTGTTACACGTGCAATCTCTTCCCTT 4099
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QY 4040 GATTAAAAATCAATAAATATCTATTACGTTTATTCACATCCCTAGTGTCTTCTTCTT 4159
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QY 4160 ATTTTATAGCACAGCTCTAATAGCAATGCAATATGCAATTCATTTAGCACTGT 4219
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QY 4220 GCTATAAATAGCAATATGTCAGTTTATTTGCTGTAAGTTTGTGTTT 4279
Db GCTATAAATAGCAATATGTCAGTTTATTTGCTGTAAGTTTGTGTTT 3898
QY 4280 GAAATATATCTTTGCTGGGTATATAAATCCATGTCATAAATCTCTTCTTCTCAGCAC 4339
Db GAAATATATCTTTGCTGGGTATATAAATCCATGTCATAAATCTCTTCTTCTCAGCAC 3958
QY 4340 TTTAATGAAGTCACTCAGTTATCTTGGCTGTATAGTTTCTGCGCTGCCTTCAAGAT 4399
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QY 4400 TTTTTCATGCTCTTAATTTTACAGTTTGTATGCTGTAGGAGTATTTCTTTGTATT 4459
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QY 4520 TCAGTTTGTGCTCTCCTCAAGTGGCTGAAAAAAGAAAAAATAAATCAAGTTT 4579
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QY 4580 AAAAAAATAATTTTGAATAATTTTCAAGTATCATTTCTTCAAATATTTATCTCTAT 4639
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QY 4700 TGTTCAGGCACTTGGATGCTGCTTCTTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 4759
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QY 4820 CTGTGAAGAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 4879
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QY 4880 CTCCTTGTCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 4930

Db 4499 CTCCTTGTCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 4558
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QY 4991 CTCCTCAACCTTCGCTCCCTGGGTTCAGAGTGATTTCTCTCGCTCATCTCTCCGAGTAG 5050
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Db	12179	GCCCGGTAAATTTATTTGTAATTTTGTAGAGATGGGGTTTCATCGTGTGCCAGGCTAG	12238	QY	13678	GGAATGTTGATTTCTAATGAACAATTACTGCTCAAAATATGGGCTGAATTTGCTGGGCTG	13737
QY	12601	TCTTGAACTCCTGAGCTCAGCGAATTCGCCGCTCTCAGTCTCCAAAGTGCCTGGGATTA	12660	Db	13319	GGAATGTTGATTTCTAATGAACAATTACTGCTCAAAATATGGGCTGAATTTGCTGGGCTG	13378
Db	12239	TCTTGAACTCCTGAGCTCAGCGAATTCGCCGCTCTCAGTCTCCAAAGTGCCTGGGATTA	12298	QY	13738	GAAATATTTGTTATTAACATTCACATGATTCAGTGTGTATTAATTTTCTTTCTTTT	13797
QY	12661	AGGCGTGAGCCACATGCCCCAGCGGCTAGCAGCTCATCTTAATCGTATATTTACTTATCTG	12720	Db	13379	AAAATATTTGTTATTAACATTCACATGATTCAGTGTGTATTAATTTTCTTTCTTTT	13438
Db	12299	AGGCGTGAGCCACATGCCCCAGCGGCTAGCAGCTCATCTTAATCGTATATTTACTTATCTG	12358	QY	13798	TTTTGACCCGATATAGATGAAGCAAGAGCAAGCAATCCCATGTGTAATAGAAAA	13857
QY	12721	GCCTTCCACAGACTGCGGGCTCTTCAAGAGTAAATGCAATGTTTCACTTTATTTCC	12780	Db	13439	TTTTGACCCGATATAGATGAAGCAAGAGCAAGCAATCCCATGTGTAATAGAAAA	13498
Db	12359	GCCTTCCACAGACTGCGGGCTCTTCAAGAGTAAATGCAATGTTTCACTTTATTTCC	12418	QY	13858	GGCAGCTGAAATGTTGTTGCTGTTTTTGAATTTTAAAGCTGGTTTTCGATTAATTCAGT	13917
QY	12781	CCAGTTGTGGCACAATCTAGGCACTCGCCATCAATGAATAAACCTCTGAGCTGTGATA	12840	Db	13499	GGCAGCTGAAATGTTGTTGCTGTTTTTGAATTTTAAAGCTGGTTTTCAATTAATTCAGT	13558
Db	12419	CCAGTTGTGGCACAATCTAGGCACTCGCCATCAATGAATAAACCTCTGAGCTGTGATA	12478	QY	13918	AAATGGTCCAGGACTAATAATGTTGAACATTTTTTACGGTGTGATTTAAATTTAGTCTT	13977
QY	12841	TTACAAACGTGGAAAGATGACGAGCACTCAGCAACTTTTCAAGTGAATGAACAAAGGCTTC	12900	Db	13559	AAATGGTCCAGGACTAATAATGTTGAACATTTTTTACGGTGTGATTTAAATTTAGTCTT	13618
Db	12479	TTACAAACGTGGAAAGATGACGAGCACTCAGCAACTTTTCAAGTGAATGAACAAAGGCTTC	12538	QY	13978	A-----TTGTTTTTTTTTTTGTGTTTTTATGATGTTTACATTTTCCCATGGGAAGCAG	14025
QY	12901	ATTGAGCATG-ATTATTTGACTGCC- AATCTGGGCTG-CTTCCGTGCTGTGGTTTCAAG	12957	Db	13619	ATAGTTTTTTTTTGGGTTTTTTTTTTTGTGTTTTTATGATGTTTACATTTTCCCATGGGAAGCAG	13678
Db	12539	ATTGAGCATGATTATTTGACTGCCCTGACTCTGGGCTGCCCTTCTCTGTCTGTGGTTTCAAG	12598	QY	14026	CTATGTCATGTCGCAATGATTCATGTTAAACATCTCGGGTATTTTGGTTTTGTGTTAT	14085
QY	12958	GAGAGCATAGCTACAGAACAGAGACCTGGCTACTCTGGAAGTTAGACTTAAGCCACCT	13017	Db	13679	CTATGTCATGTCGCAATGATTCATGTTAAACATCTCGGGTATTTTGGTTTTGTGTTAT	13738
Db	12599	GAGAGCATAGCTACAGAACAGAGACCTGGCTACTCTGGAAGTTAGACTTAAGCCACCT	12658	QY	14086	GTTCAGAAAGCGGAATGCCAAAAATAAGAGTGTTTTGTGATGCTAGTGTGCTCTCCTT	14145
QY	13018	CCGCTCCTTGAATGGGGAATATTTCCCTTCATCTCTGTTTATAGGACAGAAAGATGA	13077	Db	13739	GTTCAGAAAGCGGAATGCCAAAAATAAGAGTGTTTTGTGATGCTAGTGTGCTCTCCTT	13798
Db	12659	CCGCTCCTTGAATGGGGAATATTTCCCTTCATCTCTGTTTATAGGACAGAAAGATGA	12718	QY	14146	TACAAATCAAGGCTTTTATTTAATCCACTTAATGGGACACTCAGAAAAATTTAAAAAT	14205
QY	13078	GTAATGCAATGATACATGCTGGAATGTTTATTTCCACTACCCGAAGCTGCCTCTCAACTT	13137	Db	13799	TACAAATCAAGGCTTTTATTTAATCCACTTAATGGGACACTCAGAAAAATTTAAAAAT	13858
Db	12719	GTAATGCAATGATACATGCTGGAATGTTTATTTCCACTACCCGAAGCTGCCTCTCAACTT	12778	QY	14206	GGAAGTCCATCCACAGNAGCAGGTACTATGATGTAATAAGTTTAGTGGGGATTAAT	14265
QY	13138	AACAATCCATGAAGAAACAAAGATGTTATATACTTTTCTAATTTGTGATGCTTTGTT	13197	Db	13859	GGAAGTCCATCCACAGNAGCAGGTACTATGATGTAATAAGTTTAGTGGGGATTAAT	13918
Db	12779	AACAATCCATGAAGAAACAAAGATGTTATATACTTTTCTAATTTGTGATGCTTTGTT	12838	QY	14266	AGAGTGATCATATAATTTATGAGCTAAACCGGAGGCACTTTTTTTTTTGAGATCGAGTCT	14325
QY	13198	TATTTGTTCCGGTTTAAAGAGAGGTGGCAATGTAATGTTTGTGTTGTTGTTGTTCTTC	13257	Db	13919	AGAGTGATCATATAATTTATGAGCTAAACCGGAGGCACTTTTTTTTTTGAGATCGAGTCT	13978
Db	12839	TATTTGTTCCGGTTTAAAGAGAGGTGGCAATGTAATGTTTGTGTTGTTGTTGTTCTTC	12898	QY	14326	CACTGTTGCCCTAGGCTGGAGTGCAGTGCAGTGCAGCTCACTGCAACCTCGCCCTCC	14385
QY	13258	TTCAATAAGAGCATCTTAATAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	13317	Db	13979	CACTGTTGCCCTAGGCTGGAGTGCAGTGCAGTGCAGCTCACTGCAACCTCGCCCTCC	14038
Db	12899	TTCAATAAGAGCATCTTAATAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	12958	QY	14386	CGGTTCAAGGATTTCTCATGCTCAGCTCAGCTCAGTGCAGTGCAGTGCAGTGCAGTGCAG	14445
QY	13318	AAGTTTCGATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	13377	Db	14039	CGGTTCAAGGATTTCTCATGCTCAGCTCAGCTCAGTGCAGTGCAGTGCAGTGCAGTGCAG	14098
Db	12959	AAGTTTCGATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	13018	QY	14446	ACCATGCCAGCTAAATTTTGTGTTTTTGTAGAGATGGGTTTTTCAACATTTTGGCCAGG	14505
QY	13378	TTTATAAAGCAGAGCAGACTAGCAGTCTTTCTAATGCAATCCGCCAAATGATGATGAT	13437	Db	14099	ACCATGCCAGCTAAATTTTGTGTTTTTGTAGAGATGGGTTTTTCAACATTTTGGCCAGG	14158
Db	13019	TTTATAAAGCAGAGCAGACTAGCAGTCTTTCTAATGCAATCCGCCAAATGATGATGAT	13078	QY	14506	CTTGCTCAAACTCTGACCTCAGTGATCGCCCACTCGACCTCTTAACTCTCTGCGGA	14565
QY	13438	ATTAGATTGCTTCTCCCTATTGTTTATGATGATGATGATGATGATGATGATGATGATGAT	13497	Db	14159	CTTGCTCAAACTCTGACCTCAGTGATCGCCCACTCGACCTCTTAACTCTCTGCGGA	14218
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QY	13558	AGGGCAATGCTTTAGTTTTTAAATGTTAAATCTCAATTTTCTTTTCTTTTCTTTTCTTTT	13617	Db	14279	AGATTAATTTCTGATCTAAGTCTGAGGACCAATCAGGGCAAGCCAGATGCCATTACCACT	14338
Db	13199	AGGGCAATGCTTTAGTTTTTAAATGTTAAATCTCAATTTTCTTTTCTTTTCTTTTCTTTT	13258	QY	14686	AGCTGAAGAGCTTGCCAGGCTCATTTTACCTTGGTATATAGCAAAATTTCTTTTCTTTT	14745
QY	13618	AAGCTGTAATCACACAAGCTCTCAAGTGCAGATTTTCAATGTTGTTTTTAAACCATCTA	13677				

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Db 20038 CTAATTTTGTATTTTATAGTAGACAGAGTTTCGCCATGTTGACAGGCTTGCCCTTGA 20097
Qy 20439 CTCCTGACTTCAGGTGATCCACCCACCTCAGCCTCCAAAAGCACTGGGATTCAGGCATG 20498
Db 20098 CTCCTGACTTCAGGTGATCCACCCACCTCAGCCTCCAAAAGCACTGGGATTCAGGCATG 20157
Qy 20499 AGCCACCGTCCCGAGCCTGTTTCTCAGATCCGTGA - TTTGTTTCTGAAGCCTTCAATTC 20557
Db 20158 AGCCACCGTCCCGAGCCTGTTTCTCAGATCCGTGA - TTTGTTTCTGAAGCCTTCAATTC 20217
Qy 20558 TATCTTCTTATTTTATTTTGGAGTAGTACACCTAAAGTAAGGTTTTTAAACAATCAATATC 20617
Db 20218 TATCTTCTTATTTTATTTTGGAGTAGTACACCTAAAGTAAGGTTTTTAAACAATCAATATC 20277
Qy 20618 TTTGGAAAAATCCCTGCTTCTTTTCTTATTCCTACAAAAATATGTCAGTATAGCTGATG 20677
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Qy 20678 TTATGTTTCTTTCAAAATATTCTATCTCTCAGAAATTTATCTCATGCCCTAAATGTT 20737
Db 20338 TTATGTTTCTTTCAAAATATTCTATCTCTCAGAAATTTATCTCATGCCCTAAATGTT 20397
Qy 20738 ATTGAATAGTCTTCACTCTTGTTCATCCAGTCTTCTGCTCTTATTTCACTTAAGTCTA 20797
Db 20398 ATTGAATAGTCTTCACTCTTGTTCATCCAGTCTTCTGCTCTTATTTCACTTAAGTCTA 20457
Qy 20798 AGTGCCTATTAGATAAAGAGCTGTAAACAGATTTCTTCCAAATATGCTTATCTTTG 20857
Db 20458 ATTGCCTATTAGATAAAGAGCTGTAAACAGATTTCTTCCAAATATGCTTATCTTTG 20517
Qy 20858 ACTGCATGCCAGTGACAAACTGTTTAACTGTTTGAATCTTTCATAACATTCACAGAACAT 20917
Db 20518 ACTGCATGCCAGTGACAAACTGTTTAACTGTTTGAATCTTTCATAACATTCACAGAACAT 20577
Qy 20918 GCTGACTCTCTCTTCTCTGAAAGCAATGCCCAAGCAGCAAGATTTGTAGATAGTATGACG 20977
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Db 20698 GTGATATGGTCTGCTGACTTAGACTCCAAAGGCTGCTGAGGTGAAACACACATCTGCCAT 20757
Qy 21098 ACCCAGGAAGCACACAGGTGGATGGAAGAGCTGTGCTTAATGAAACTTCAACCTGG 21157
Db 20758 ACCCAGGAAGCACACAGGTGGATGGAAGAGCTGTGCTTAATGAAACTTCAACCTGG 20817
Qy 21158 AGGTGGAGGAGGTGCTGAGCTGCAAGAACTCAGAGCTGCTTACCCAGACAGGACCCAGG 21217
Db 20818 AGGTGGAGGAGGTGCTGAGCTGCAAGAACTCAGAGCTGCTTACCCAGACAGGACCCAGG 20877
Qy 21218 GAGGCTTTCTGGAGGAAACAGCCTCTGAACTGCCAGCTCATAGAGAGCTCTACCTCAA 21277
Db 20878 GAGGCTTTCTGGAGGAAACAGCCTCTGAACTGCCAGCTCATAGAGAGCTCTACCTCAA 20937

QY	30024	TATGATCTTTCTTGTCATAGGAAATTCATAGTGATTTCCCATCACCCCTTGGGATTATC	30083	Db	30774	TGGTGTCTGGGAAGGCCCAATTTGCTCATAGATGGAGCATGACCTTTCACTCTCTGTGCA	30833
Db	29695	TATGATCTTTCTTGTCATAGGAAATTCATAGTGATTTCCCATCACCCCTTGGGATTATC	29754	QY	31164	CATGGCAGAGGGCAAGAGAGCTCTCTGGGTCTTTTTTATAAGGGCACTAATCTCATTTT	31223
QY	30084	ATAGCTCCCTTAAAGTCCCTCTATGCACTCANTACATCAACAGTAAGTGTCTTCGAG	30143	Db	30834	CATGGCAGAGGGCAAGAGAGCTCTCTGGGTCTTTTTTATAAGGGCACTAATCTCATTTT	30893
Db	29755	ATAGCTCCCTTAAAGTCCCTCTATGCACTCANTACATCAACAGTAAGTGTCTTCGAG	29814	QY	31224	TGAGGACCTCCCTCCCATGACTTAATCACTCTCCCAAGGGCACTGTCTCCCAATACCATCA	31283
QY	30144	CACCTACTAGTGATATATCATTTGTCTCACGACGACCCACAGACTCTCACCAAGAAC	30203	Db	30894	TGAGGACCTCCCTCCCATGACTTAATCACTCTCCCAAGGGCACTGTCTCCCAATACCATCA	30953
Db	29815	CACCTACTAGTGATATATCATTTGTCTCACGACGACCCACAGACTCTCACCAAGAAC	29874	QY	31284	CCTTAGAGGTTAGGATTTCAACATATGATTTGGGGGGGACAGAAACACGAGTCCATCTC	31343
QY	30204	TAGCTGAGCCCTGAGAAATAGTAAGTAAGTACTGCCATGCCAATCTGAGTACTCAAGC	30263	Db	30954	CCTTAGAGGTTAGGATTTCAACATATGATTTGGGGGGGACAGAAACACGAGTCCATCTC	31013
Db	29875	TAGCTGAGCCCTGAGAAATAGTAAGTAAGTACTGCCATGCCAATCTGAGTACTCAAGC	29934	QY	31344	GCCTGTCCACTCCATGTGGTATTTCTGCTGGATCAGTTCCTCTCTGGGGTGCATTTGT	31403
QY	30264	GATGCAAAATGATTCCTTTAATTTACTTTTGAGGCTTCTGAGTTTGTCTATGGAGAG	30323	Db	31014	GCCTGTCCACTCCATGTGGTATTTCTGCTGGATCAGTTCCTCTCTGGGGTGCATTTGT	31073
Db	29935	GATGCAAAATGATTCCTTTAATTTACTTTTGAGGCTTCTGAGTTTGTCTATGGAGAG	29994	QY	31404	GTTCCATGTCTAATTCGAAATTTAGCAGCCCGATAGCAAAAGTATTTCCAAATTTGGTA	31463
QY	30324	TGCTACTGATCCATGTTATATCTATGTAAATTTGGATCGGAGACATCACTTGACTTT	30383	Db	31074	GTTCCATGTCTAATTCGAAATTTAGCAGCCCGATAGCAAAAGTATTTCCAAATTTGGTA	31133
Db	29995	TGCTACTGATCCATGTTATATCTATGTAAATTTGGATCGGAGACATCACTTGACTTT	30054	QY	31464	TGCAGAGGCAATGAATTAATCAGATGAACCCAGCCCAACCACTGCTAGAGCTGCAGA	31523
QY	30384	TTCCAGAGCAAAATACAGCTGATGACAAAGCTGCTGAGAAATGGATATTTTCTGA	30443	Db	31134	TGCAGAGGCAATGAATTAATCAGATGAACCCAGCCCAACCACTGCTAGAGCTGCAGA	31193
Db	30055	TTCCAGAGCAAAATACAGCTGATGACAAAGCTGCTGAGAAATGGATATTTTCTGA	30114	QY	31524	GAGTACCAGCTGATTTATGAGCCCTGGTAAACAGTGGTTTTAGTTCCTATGCTCGTCAGC	31583
QY	30444	ATTGAGTTTACGTGGAAACAGCTGACTAGTTTCCATTTCTGTAAGAAATGGCTTTTTCG	30503	Db	31194	GAGTACCAGCTGATTTATGAGCCCTGGTAAACAGTGGTTTTAGTTCCTATGCTCGTCAGC	31253
Db	30115	ATTGAGTTTACGTGGAAACAGCTGACTAGTTTCCATTTCTGTAAG - ATGGCTCTTTTCG	30173	QY	31584	CCTTTCTCCATAGTAGCCCACTGTGTGAAGTGGCTGAATCGACAGAGCTTCAGC	31643
QY	30504	TCTTGTCTGATTTGAGTAATGGCTTACTTCTGTAGAAGAGAGATTTCAATTTGAGTCC	30563	Db	31254	CCTTTCTCCATAGTAGCCCACTGTGTGAAGTGGCTGAATCGACAGAGCTTCAGC	31313
Db	30174	TCTTGTCTGATTTGAGTAATGGCTTACTTCTGTAGAAGAGAGATTTCAATTTGAGTCC	30233	QY	31644	TTGGGCCACATGCTCATGGAACCAATTCCTTATGAGCCGTACAAGAGCTGGGTGCGCA	31703
QY	30564	ACTCAGGATTTGGTTTCAACAAACTGGAGTACAGGTTTTCAGAAATATCTCTTTAATGCT	30623	Db	31314	TTGGGCCACATGCTCATGGAACCAATTCCTTATGAGCCGTACAAGAGCTGGGTGCGCA	31373
Db	30234	ACTCAGGATTTGGTTTCAACAAACTGGAGTACAGGTTTTCAGAAATATCTCTTTAATGCT	30293	QY	31704	TTCTGGATACCTCTTTTTCAGAGATTTTATTTCAAGGATATTTTCTTTTATCAAC	31763
QY	30624	CCAATAATAATTTCTCATATTAATTCCTGGAACACTTCAATCTTGTGACGCGAGCAT	30683	Db	31374	TTCTGGATACCTCTTTTTCAGAGATTTTATTTCAAGGATATTTTCTTTTATCAAC	31433
Db	30294	CCAATAATAATTTCTCATATTAATTCCTGGAACACTTCAATCTTGTGACGCGAGCAT	30353	QY	31764	TACAGGATTTATTTAGAAATCTTAGGGCAGTGGTCCCAACCTTTTGGCCCGAGGACAG	31823
QY	30684	ATAGATAGATTTGTTGCTCACTGTGTCTGATTTGACCTTTTCACTGCTTTTCAACTTA	30743	Db	31434	TACAGGATTTATTTAGAAATCTTAGGGCAGTGGTCCCAACCTTTTGGCCCGAGGACAG	31493
Db	30354	ATAGATAGATTTGTTGCTCACTGTGTCTGATTTGACCTTTTCACTGCTTTTCAACTTA	30413	QY	31824	GTTTGTGGGAGACAGTTTTCATGGAACAGTGTACAGGGGGCTGGGAGGATGGTTTTG	31883
QY	30744	GGTTACAAATAGAACAGAAATCTCTGATTTTCTCATTAATTTGTTGAATTTCCACTTT	30803	Db	31494	GTTTGTGGGAGACAAATTTTTCATGGAACAGTGTACAGGGGGCTGGGAGGATGGTTTTG	31553
Db	30414	GGTTACAAATAGAACAGAAATCTCTGATTTTCTCATTAATTTGTTGAATTTCCACTTT	30473	QY	31884	GGATGCTCAAGTACATTTGTTGATATCTTTTCTATTTCTATTTATTTATTTGTA	31943
QY	30804	TCTCATTAGCAAGAGTCCAGTACTTCTGAGAACTTCTTCTGATTTTCTCAATCTAGAACT	30863	Db	31554	GGATGCTCAAGTACATTTGTTGATATCTTTTCTATTTCTATTTATTTATTTGTA	31613
Db	30474	TCTCATTAGCAAGAGTCCAGTACTTCTGAGAACTTCTTCTGATTTTCTCAATCTAGAACT	30533	QY	31944	TATATAATGAAATTAATTTACACAACTCACCAATATGTAGGAATCAGTGGGAGGCTTAAGT	32003
QY	30864	TACTTGGTCCATAAGGTAACAGTCTTATTTCTGACTATCAAGGAGAGAAATAACAGGAGC	30923	Db	31614	TATATAATGAAATTAATTTACACAACTCACCAATATGTAGGAATCAGTGGGAGGCTTAAGT	31671
Db	30534	TACTTGGTCCATAAGGTAACAGTCTTATTTCTGACTATCAAGGAGAGAAATAACAGGAGC	30593	QY	32004	TTGTTTTCTGCAACTAGACAGTCCCAATCTGGGGGCAATGGGAGATAGTGAAGATCATC	32063
QY	30924	CATTATCATCTTCAGGTGTCTTTTGAATACTGGTCTCTGTAGATCTTCAGATTCTT	30983	Db	31672	TTGTTTTCTGCAACTAGACAGTCCCAATCTGGGGGCAATGGGAGATAGTGAAGATCATC	31731
Db	30594	CATTATCATCTTCAGGTGTCTTTTGAATACTGGTCTCTGTAGATCTTCAGATTCTT	30653	QY	32064	AAGCATTAGATTCTCATAGGAGTGTCTCAGCTTAGATCCCGGCACTGTGCAGTTCAAT	32123
QY	30984	GGTTAGTCCATTACAGTCTTATACAAATTTGCATAGACAGATGGCTTTATTAATAACA	31043	Db	31732	AAGCATTAGATTCTCATAGGAGTGTCTCAGCTTAGATCCCGGCACTGTGCAGTTCAAT	31791
Db	30654	GGTTAGTCCATTACAGTCTTATACAAATTTGCATAGACAGATGGCTTTATTAATAACA	30713	QY	32124	AGGATTTGCTCACTATGAAATCTTAATGCCATGTGTATCTGACAGGAGGTGAGCTCG	32183
QY	31044	GAAATGATTTCTGACAGTTCTGAAGGCTGAGAAATCAAGAGTAAAGACATGGCTGATT	31103	Db	31792	AGGATTTGCTCACTATGAAATCTTAATGCCATGTGTATCTGACAGGAGGTGAGCTCG	31851
Db	30714	GAAATGATTTCTGACAGTTCTGAAGGCTGAGAAATCAAGAGTAAAGACATGGCTGATT	30773	QY	32184	GGCAGTAAATCGAGGGTTGGGAGCAGCTGTCAATATAGATGAAGCTTTTCTGCTCGCC	32243
QY	31104	TGGTGTCTGCGAAGGCCCATTTGCTCATAGATGGACGATGACCTTTCACTCTGTCTGCA	31163				

Db 31852 GCAGTAATGCGAGGTTGGGAGCAGCTGTCAAATAGATGAAGCTTTGCTCGCTCGCC 31911
Qy 32244 TGCCATCACTCCTCTGCTGTGTGTCACCTTCTTAACAGGTCAACAGCTGTGCTGCTCC 32303
Db 31912 TGCCATCACTCCTCTGCTGTGTGTCACCTTCTTAACAGGTCAACAGCTGTGCTGCTCC 31971
Qy 32304 ATGGCAGGAGTTGGGAGCCCTCTTATAGGAGTAGGGGTGAGTTCCTTCACTTCTA 32363
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Qy 32364 GAAGGCCCTGGATATGATATCCAGAGCTGTCAATACAGAGTATCAAAACAGGTGGCTA 32423
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Qy 32784 CATATCTTTTGAAGAACACAGTTCAACCAATAGAGCCCTGTACTGTTTACAAATAG 32843
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Qy 33019 ATGCTGTAATCCAGACCTTTGGGAAATAGAGGAGTGGATCAACCTTGAAGTCAAGAG 33078
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Qy 33559 GAAAAAATAAAAAAAGCTGGGTGTGCTTTATGCTGTAGTCTCAGTACC 33618
Db 33230 G - AAAAAAATAAAAAAAGCTGGGTGTGCTTTATGCTGTAGTCTCAGTACC 33288
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Db 37425 AACTGGAAAGTAGTTTCAGGCCAGAGCTAGGAAATTCACCCATCTCCAGGTCTCAGGTCTG 37484
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Db 37485 CAAGGGAGGCTCAGCTTAAACATGAGGAGCTAGAAAATTTGTGCTGGAGCTTGCACCAAC 37544
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AUTHORS Barry,A.E., Bateman,M., Howman,E.V., Cancilla,M.R., Tainton,K.M.,
Irvine,D.V., Saifery,R. and Choo,K.H.
TITLE The 10q25 neocentromere and its inactive progenitor have identical
primary nucleotide sequence: further evidence for epigenetic
modification
JOURNAL Genome Res. 10 (6), 832-838 (2000)
MEDLINE 20314874
PUBMED 10854414
REFERENCE 2 (bases 1 to 80202)
AUTHORS Barry,A.E.
TITLE Direct Submission
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Institute, 10th Floor, Royal Childrens Hospital, Flemington Rd.,
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REMARK Human genomic sequence from 10q25.2, clonelib=NC, second release
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Db 3419 TAGTCCAGCTACTTTGGAGGCTGAGGAGGAGAAATCTCTTGAACCCGGGAAGGGAGGT 3478
Qy 3860 TACAGTGAACCAAGTTGCTCCTACTGCACTGCACTGAGCTGGGCAACAGAGTGTCTC 3919
Db 3479 TACAGTGAACCAAGTTGCTCCTACTGCACTGCACTGAGCTGGGCAACAGAGTGTCTC 3538
Qy 3920 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3979
Db 3539 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3598
Qy 3980 TATATCTCATGCTTAGCTTGCACACCTTGTGTTTACACTGTCAGTGTACCTTCTAAGA 4039
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Qy 4040 GATTAAAAATCAATAAATATCTATGCTTATTCACATCTCAGTGTATTTCTTCTT 4099
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Qy 4220 GCTATAAAATAGCAATGCAATTTATTTTATTTGCTGAAAAAGTTTGTGTTTTT 4279
Db 3839 GCTATAAAATAGCAATGCAATTTATTTTATTTGCTGAAAAAGTTTGTGTTTTT 3898
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Db 3899 GAAATATATCTTTCTGGGTATATAAATCCATGTGCAATCTCTTTTCTTCTGAGCAC 3958
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Qy 4400 TTTTTCATGTCTTAAATTTTACAGTTTGTATGTCCTAGGAGTGTATTTCTTGTAT 4459
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Qy 4820 CTGTTGAAGAAATCTTTTGTCTTTTAAATATCATGTTTTTATTTCTAGCATTTTCACTG 4879
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Db	9999	AAAGCTCCAAAATGATTAGCGGCTGACGGATTGATTATTAAGAAATTTAAAGAAAT	9658	QY	11106	GAGGCGAGAGGTGCTGATTAGCAGCTGACCCGCCCTCTTTCTGTCCTCAITTCGTGG	11165
QY	10026	AAATGTGTATAGCTCAGCTAAGCAAGATGAAAGAGACCAAGCTAAATGTATACAAATATC	10085	Db	10739	GAGGCGAGAGGTGCTGATTAGCAGCTGACCCGCCCTCTTTCTGTCCTCAITTCGTGG	10798
Db	9659	AAATGTGTATAGCTCAGCTAAGCAAGATGAAAGAGACCAAGCTAAATGTATACAAATATC	9718	QY	11166	AAAATTGAGTGGAGCTCAATTTTGGTGGAGCTCTAAGTAGTCTCACTTTGAGACATTGA	11225
QY	10086	TGAAACGTGCAGAACTTTAAAGAGAGATTAAATTTTAAACATGATACACGGGGGACAA	10145	Db	10799	AAAATTGAGTGGAGCTCAATTTTGGTGGAGCTCTAAGTAGTCTCACTTTGAGACATTGA	10958
Db	9719	TGAAACGTGCAGAACTTTAAAGAGAGATTAAATTTTAAACATGATACACGGGGGACAA	9778	QY	11226	GTGGAGCTCTAAGTCTCTCAGAAATAGCAAAACACTAGTTTCTTTTCTTTTCTTTT	11285
QY	10146	TATGCACTCAGAGATGAAATTTTCACTCAGTATCTAGAGAAATTTCCCGATAGTGAAT	10205	Db	10859	GTGGAGCTCTAAGTCTCTCAGAAATAGCAAAACACTAGTTTCTTTTCTTTTCTTTT	10918
Db	9779	TATGCACTCAGAGATGAAATTTTCACTCAGTATCTAGAGAAATTTCCCGATAGTGAAT	9838	QY	11286	TTTTTTTTTGGAGACAGAGTCTTGCTGCTCGCCAGGCTGGAGTGCATGGCAGATCT	11345
QY	10206	CTGTTAAGGCTGTCTGATGTGGCTTTCCCTGGAGAGCAATAGAAATTTCAAGTCTT	10265	Db	10919	TTTTTTTTTGGAGACAGAGTCTTGCTGCTCGCCAGGCTGGAGTGCATGGCAGATCT	10978
Db	9839	CTGTTAAGGCTGTCTGATGTGGCTTTCCCTGGAGAGCAATAGAAATTTCAAGTCTT	9898	QY	11346	CCGCTCACTGAACCTGCTCCCGGTTCAAGCGACTCTCTGCTCAGCTCAGCTCCCGAGTA	11405
QY	10266	ACGATTTTAAAGTTTCTTGGAACTAGGTATTAGATGATTTAGAGAAATTTATTAAT	10325	Db	10979	CCGCTCACTGAACCTGCTCCCGGTTCAAGCGACTCTCTGCTCAGCTCAGCTCCCGAGTA	11038
Db	9899	ACGATTTTAAAGTTTCTTGGAACTAGGTATTAGATGATTTAGAGAAATTTATTAAT	9958	QY	11406	GCTGGATTACAGGTGCCACACACACCGCCAGCTAAATTTTCTATTTTATAGTAGAGATG	11465
QY	10326	TTGCTCAGGTATGATTAATGTATTGTAGTTCTATAAGAAAAATTTTATTTTATAGTTA	10385	Db	11039	GCTGGATTACAGGTGCCACACACACCGCCAGCTAAATTTTCTATTTTATAGTAGAGATG	11098
Db	9959	TTGCTCAGGTATGATTAATGTATTGTAGTTCTATAAGAAAAATTTTATTTTATAGTTA	10018	QY	11466	AGGTTTACCGTGTGGCAGGCTGGTCTCAAACTCTGGGCTCAAGTGTCCGCTGCC	11525
QY	10386	CATACCTGAAATATAGCATAGATATGATGTAGGAGATTGCTTTTAAATACCCACGT	10445	Db	11099	AGGTTTACCGTGTGGCAGGCTGGTCTCAAACTCTGGGCTCAAGTGTCCGCTGCC	11158
Db	10019	CATACCTGAAATATAGCATAGATATGATGTAGGAGATTGCTTTTAAATACCCACGT	10078	QY	11526	TTGGCTCCCAAGTCTCTGGGATTACAGGTGTGAGCCACACACCCAGCTCAGAAACCT	11585
QY	10446	AAGGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10505	Db	11159	TTGGCTCCCAAGTCTCTGGGATTACAGGTGTGAGCCACACACCCAGCTCAGAAACCT	11218
Db	10079	AAGGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10138	QY	11586	ATTTTCTTGAATGGAGAAACACTTTCCCTTATTTATTTAGTTTGGGAGCAAGAGAG	11645
QY	10506	AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10565	Db	11219	ATTTTCTTGAATGGAGAAACACTTTCCCTTATTTATTTAGTTTGGGAGCAAGAGAG	11278
Db	10139	AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10198	QY	11646	GGTAAATCAATTAAGTGAATAATTTCCAAATCCAGAAACATCGATAAGCAGCAGCTTA	11705
QY	10566	TCATGCCCTAATATCCAGCACTTTAGGAGGCCAAGTTGGAGGATCACTTAATTAAGCCCA	10625	Db	11279	GGTAAATCAATTAAGTGAATAATTTCCAAATCCAGAAACATCGATAAGCAGCAGCTTA	11338
Db	10199	TCATGCCCTAATATCCAGCACTTTAGGAGGCCAAGTTGGAGGATCACTTAATTAAGCCCA	10258	QY	11706	ATTTTCTTGAAGGAGAAATTTTAAACATATCTTTTGAAGCTCTTTTGAAGAGCCTCA	11765
QY	10626	GGAGTTCAGGCTGCAGTGTGATGCGCCACTGCACCTCCAGCTGGGTGGCAGAG	10685	Db	11339	ATTTTCTTGAAGGAGAAATTTTAAACATATCTTTTGAAGCTCTTTTGAAGAGCCTCA	11398
Db	10259	GGAGTTCAGGCTGCAGTGTGATGCGCCACTGCACCTCCAGCTGGGTGGCAGAG	10318	QY	11766	CGTCTTCCCTTGAATGTGAGAGTGGGAAATCCAGGGA-CTTTTGGAAATCGATGCCCTTA	11824
QY	10686	TGAAGCCCTGTCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10745	Db	11399	CGTCTTCCCTTGAATGTGAGAGTGGGAAATCCAGGAGGTTTGGAAATCGATGCCCTTA	11458
Db	10319	TGAAGCCCTGTCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10378	QY	11825	TGCTGCTTTTGTGTTTGTAGAGAAATATAATATTTTATCTAGGTTTCTGATGGCA	11884
QY	10746	ATGCAAGATGTTGGTAAATGGAACCTGAAGGAGTTAATATGAGTTCACCTTTCCCTC	10805	Db	11459	TGCTGCTTTTGTGTTTGTAGAGAAATATAATATTTTATCTAGGTTTCTGATGGCA	11518
Db	10379	ATGCAAGATGTTGGTAAATGGAACCTGAAGGAGTTAATATGAGTTCACCTTTCCCTC	10438	QY	11885	GTCAGCATGAAACACCACTGTTGAGAGCTGTAATTTCTGAAATTTCTGAGAGTG	11944
QY	10806	TTCAAGTCTCTTATGATGTTTGGCACTTTTCAATTAAGCAATTTAAATATATTTTC	10865	Db	11519	GTCAGCATGAAACACCACTGTTGAGAGCTGTAATTTCTGAAATTTCTGAGAGTG	11578
Db	10439	TTCAAGTCTCTTATGATGTTTGGCACTTTTCAATTAAGCAATTTAAATATATTTTC	10498	QY	11945	CACATCTAGGCCAGCAATGGCAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	12004
QY	10866	CTGATCAAACTTAGTAGAGTATTAAATCCCTGGGCTTCTGACTAGAACAGCCTCATTA	10925	Db	11579	CACATCTAGGCCAGCAATGGCAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	11638
Db	10499	CTGATCAAACTTAGTAGAGTATTAAATCCCTGGGCTTCTGACTAGAACAGCCTCATTA	10558	QY	12005	ACTCAGAACCAATCGGCTCTGACTGAAAGTGAAGCGGAGCGGCTGTGTGGGAAAGCTGG	12064
QY	10926	CCACATGGGAGAGTTCTGGCCGACAGGAGCACCGTAGTGGTTACCATCTGTGCTGG	10985	Db	11639	ACTCAGAACCAATCGGCTCTGACTGAAAGTGAAGCGGAGCGGCTGTGTGGGAAAGCTGG	11698
Db	10559	CCACATGGGAGAGTTCTGGCCGACAGGAGCACCGTAGTGGTTACCATCTGTGCTGG	10618	QY	12065	CTGAGTCTCTCTATAGCAGGAGTCTTTTCTCCAGCCGCTCACTGTGTTGTTGG	12124
QY	10986	TAATGTGGTCTGGGCTGAAGGGCCCTTTCTAAGTTGTAGATAGAAATCCAGGAACTTG	11045	Db	11699	CTGAGTCTCTCTATAGCAGGAGTCTTTTCTCCAGCCGCTCACTGTGTTGTTGG	11758
Db	10619	TAATGTGGTCTGGGCTGAAGGGCCCTTTCTAAGTTGTAGATAGAAATCCAGGAACTTG	10678	QY	12125	GCCACGTAAGCTCTCTGAGCTTAGGCTGTAAACCCCCACCACTCTCTCTCTGCTGCC	12184
QY	11046	TTAGAACTGCAGACCTATCAGGGTACCTGCAGGAGGTGAGTCTACTAAGGTGAAAAAGCA	11105				

Db 16138 CTATTCTCCGCAAACTGGCAGAGGTAAGTGAGACTGCGGAAGAGCAAGTTTTCGAAGTC 16197
Qy 16541 CAGAGGAATGAAGACTCTGCTTTCGCACATGCTGGGTTTGACGGTGTGATATCCGA 16600
Db 16198 CAGAGGAATGAAGACTCTGCTTTCGCACATGCTGGGTTTGACGGTGTGATATCCGA 16257
Qy 16601 TGATGCGCCCTTAAGGTGAGCTCAAGCTTTAAGGAGAGATAGGGGCTGATGATCTGAGA 16660
Db 16258 TGAATGCGCCCTTAAGGTGAGCTCAAGCTTTAAGGAGAGATAGGGGCTGATGATCTGAGA 16317
Qy 16661 TTCAATCAGTGTGGGTGATGTTTAAACCCAGGGGACAGATAAGAGGTTTATCCAGGG 16720
Db 16318 TTCAATCAGTGTGGGTGATGTTTAAACCCAGGGGACAGATAAGAGGTTTATCCAGGG 16377
Qy 16721 AGAGCGTAGATAAGAGCTAAATGCTTCTGGGCTCTTAGTCATTCAAAAATCGGACCTC 16780
Db 16378 AGAGCGTAGATAAGAGCTAAATGCTTCTGGGCTCTTAGTCATTCAAAAATCGGACCTC 16437
Qy 16781 TGAGGAGGAGGAAAGCCCAAGAAAGTAGATTCTCGGACTCACGGGATTAAGACTTTTC 16840
Db 16438 TGAGGAGGAGGAAAGCCCAAGAAAGTAGATTCTCGGACTCACGGGATTAAGACTTTTC 16497
Qy 16841 AAAAAGTGGGGCTGGCCAGTGTGCTGAAGGAAGTAGCAGGACCGACAGAGGGTAA 16900
Db 16498 AAAAAGTGGGGCTGGCCAGTGTGCTGAAGGAAGTAGCAGGACCGGAAACAGAGGGTAA 16557
Qy 16901 TCGTTGACCTGGAGAACTTGAATTTGAATTTTGAAGTTTGGTAACCTTAAAAAAGAGCAA 16960
Db 16558 TCGTTGACCTGGAGAACTTGAATTTGAATTTTGAAGTTTGGTAACCTTAAAAAAGAGCAA 16617
Qy 16961 TTTTAGTACCTTTGAAATTTATTCGAAGATTGTTTGGTATATGTGTATATTCAGGCA 17020
Db 16618 TTTTAGTACCTTTGAAATTTATTCGAAGATTGTTTGGTATATGTGTATATTCAGGCA 16677
Qy 17021 AAGGACACAGAAAGTAAAAAATACTTACTGAACAGTTACTGATCGCTGGCACTGTAAC 17080
Db 16678 AAGGACACAGAAAGTAAAAAATACTTACTGAACAGTTACTGATCGCTGGCACTGTAAC 16737
Qy 17081 ACCCTGTTTAAATCTCAGGCAACCCCTATAGAGTAGGTGTCATCATCCCCATCTTACAGA 17140
Db 16738 ACCCTGTTTAAATCTCAGGCAACCCCTATAGAGTAGGTGTCATCATCCCCATCTTACAGA 16797
Qy 17141 TGAGGATAGAGTGACGTAGATTAAAGAGTTTGGCTCAGGTTTACACCAACTGGTTAAC 17200
Db 16798 TGAGGATAGAGTGACGTAGATTAAAGAGTTTGGCTCAGGTTTACACCAACTGGTTAAC 16857
Qy 17201 GTAGAGCTAGGATTGAACCCGATGGGCTGATCCAGAGCTCATGCTTTAAATCGCTAG 17260
Db 16858 GTAGAGCTAGGATTGAACCCGATGGGCTGATCCAGAGCTCATGCTTTAAATCGCTAG 16917
Qy 17261 ACTGGTCTCACAAGACCTGGGACCGAAAAAATTAATAAAAAAATTAAGGCCCCCT 17320
Db 16918 ACTGGTCTCACAAGACCTGGGACCGAAAAAATTAATAAAAAAATTAAGGCCCCCT 16977
Qy 17321 GGGCTAGCAAAATAGGAGTTGTTTACAGACATGTGAAAAGGAAAGCAAGCAGAGGAAA 17380
Db 16978 GGGCTAGCAAAATAGGAGTTGTTTACAGACATGTGAAAAGGAAAGCAAGCAGAGGAAA 17037
Qy 17381 GTCACTGTAAGAGAGAGAGACCCATGACAGAGAGACAGTGAAGTGAAGTGGCTG 17440
Db 17038 GTCACTGTAAGAGAGAGAGACCCATGACAGAGAGACAGTGAAGTGAAGTGGCTG 17097
Qy 17441 GCGATCTAGCCCTGAAAAATACCTCCAGAGAGGAGGCTCACGCCCTGTAAATCCAGCACT 17500
Db 17098 GCGATCTAGCCCTGAAAAATACCTCCAGAGAGGAGGCTCACGCCCTGTAAATCCAGCACT 17157
Qy 17501 TTGGAGCGCGAGGTGGGAGATCACTGAGGTCAGAGGTTTACAGACCGAGCTGGCCAAAT 17560
Db 17158 TTGGAGCGCGAGGTGGGAGATCACTGAGGTCAGAGGTTTACAGACCGAGCTGGCCAAAT 17217
Qy 17561 GGGCAAAATCCGCTCTCTACTAAAAAATTAAGCCAGAGCATGGTGACAGGACCTG 17620
Db 17218 GGGCAAAATCCGCTCTCTACTAAAAAATTAAGCCAGAGCATGGTGACAGGACCTG 17277

Qy 17621 TAATCCAGCTGTTTCAGTTGGCTGAGTCAGGAATAGCCTGGATCCGGGAAGTGGAGGT 17680
Db 17278 TAATCCAGCTGTTTCAGTTGGCTGAGTCAGGAATAGCCTGGATCCGGGAAGTGGAGGT 17337
Qy 17681 TGTAGTAAGCAAGATTGCGCCACTGCTGATCCAGCTGGGCGACAGAGCAGACTTTTCT 17740
Db 17338 TGTAGTAAGCAAGATTGCGCCACTGCTGATCCAGCTGGGCGACAGAGCAGACTTTTCT 17397
Qy 17741 TAAACCAAAACAAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 17800
Db 17398 TAAACCAAAACAAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 17457
Qy 17801 GAGAGAAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 17860
Db 17458 GAGAGAAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 17517
Qy 17861 GAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 17920
Db 17518 GAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 17577
Qy 17921 CCTCCAGAGGAGGAGGCTCTCTTAGGCTTCTGAGAACTCACATCCCTTTTGTGAAAC 17980
Db 17578 CCTCCAGAGGAGGAGGCTCTCTTAGGCTTCTGAGAACTCACATCCCTTTTGTGAAAC 17637
Qy 17981 AAATGCTTACACTCTCAATGTTATTGGTAAATCCAGTTTCAATATACCTTAATCATT 18040
Db 17638 AAATGCTTACACTCTCAATGTTATTGGTAAATCCAGTTTCAATATACCTTAATCATT 17697
Qy 18041 AGTACTGAATCTGGCATATAGTAATCACCTTAATGAAGAGATAAGAGTCACTGGAGTATCT 18100
Db 17698 AGTACTGAATCTGGCATATAGTAATCACCTTAATGAAGAGATAAGAGTCACTGGAGTATCT 17757
Qy 18101 GAAGCAATTAAGATTAAGTAAATATATACATATACATGAGCAACAAAGTTGGATCTTAA 18160
Db 17758 GAAGCAATTAAGATTAAGTAAATATATACATATACATGAGCAACAAAGTTGGATCTTAA 17817
Qy 18161 CGACTCAGTGAAAGAAAGGAAAGGAAAGATACATACACCGGTACCATTTATGTTAAATGAT 18220
Db 17818 CGACTCAGTGAAAGAAAGGAAAGGAAAGATACATACACCGGTACCATTTATGTTAAATGAT 17877
Qy 18221 AATATATGCTTACAAATTTGTAAAGACACATACAAATAGATACATGATATTTAAATATA 18280
Db 17878 AATATATGCTTACAAATTTGTAAAGACACATACAAATAGATACATGATATTTAAACATA 17937
Qy 18281 CTCGAAAGGTTA-CCTATGGGCTGGCTGGAGTGGGCTTAAGTCCGTAAGCTGTAATG 18339
Db 17938 CTCGAAAGGTTTACCTATGGGCTGGCTGGAGTGGGCTTAAGTCCGTAAGCTGTAATG 17997
Qy 18340 GAACTTAAACAAATACATGAAACCGAGTAGGAATCAGAAGGAGTAACAAATAAAAATGTGCC 18399
Db 17998 GAACTTAAACAAATACATGAAACCGAGTAGGAATCAGAAGGAGTAACAAATAAAAATGTGCC 18057
Qy 18400 ATGAATCGAGAGGTGTAATTAATCAACTCAGTCACTGAGTTAGGTTAAAGTAAAGAGATG 18459
Db 18058 ATGAATCGAGAGGTGTAATTAATCAACTCAGTCACTGAGTTAGGTTAAAGTAAAGAGATG 18117
Qy 18460 ATAATTTGTTATTTTACTCGTAGGCTTTCACCTTGCATCAGCTTTTACAATTTTGA 18519
Db 18118 ATAATTTGTTATTTTACTCTTAGTCTTCCATCTTGCATCAGCTTTTACAATTTTGA 18177
Qy 18520 CTATCTTTCAGATGGACCTCTTTCAGTCTTTCAGTCTGAGGAGGAGCTTTTCTCCAGC 18579
Db 18178 CTATCTTTCAGATGGACCTCTTTCAGTCTTTCAGTCTGAGGAGGAGCTTTTCTCCAGC 18237
Qy 18580 TTTCTAGTGTATTAATATATATATATATATATATATATATATATATATATATATATAT 18639
Db 18238 TTTCTAGTGTATTAATATATATATATATATATATATATATATATATATATATATATAT 18297
Qy 18640 TAGCCTTTCTGAGCTTCAGAGCTTAAATGCAAGTCAAGTTTACATGATGATTTCTCT 18699
Db 18298 TAGCCTTTCTGAGCTTCAGAGCTTAAATGCAAGTCAAGTTTACATGATGATTTCTCT 18357

QY	18700	ATGAAATTAGGCAAGGTAGAAACTGGCACAGAAAAATGTGATTTATTATGGTGTAC	18759	Db	19438	CCCACTGGATAAAGAACATTCGCATATCTCAATGACACCTTTTCTCAGGTGGGATG	19497
Db	18358	ATGAAATTAGGCAAGGTAGAAACTGGCACAGAAAAATGTGATTTATTATGGTGTAC	18417	QY	19839	GTAGATGCTGGAATGGGTACAGCATTCGCCCAACAACTTTGCAAAAAGGCTGGAGC	19898
QY	18760	TATCCCTTACAAGGAGTGTACGCTGCTTTTGTGTCACATGATTAAGCAAGATCA	18819	Db	19498	GTAGATGCTGGAATGGGTACAGCATTCGCCCAACAACTTTGCAAAAAGGCTGGAGC	19557
Db	18418	TATCCCTTACAAGGAGTGTACGCTGCTTTTGTGTCACATGATTAAGCAAGATCA	18477	QY	19899	TCTGACTGGGACCTAAATATGCAAAAGTTGATAGGCTCTTCATGAGATAATGAACC	19958
QY	18820	ACTGAAAGTGGCTATGATCACGCTTTCAAAAGCACACTCTGGCCCTCGGCTGCAGGCGC	18879	Db	19558	TCTGACTGGGACCTAAATATGCAAAAGTTGATAGGCTCTTCATGAGATAATGAACC	19617
Db	18478	ACTGAAAGTGGCTATGATCACGCTTTCAAAAGCACACTCTGGCCCTCGGCTGCAGGCGC	18537	QY	19959	CGTGTATGATATAGCTAAAGGGTGGCCCTTATGTTTCTATTCCTTACAAAACCTGGTA	20018
QY	18880	CTTGCAATTTCCCGAGCTGGGTGTCCGGTGTGACACAGTGCATAATGTGGCGCTTCC	18939	Db	19618	CGTGTATGATATAGCTAAAGGGTGGCCCTTATGTTTCTATTCCTTACAAAACCTGGTA	19677
Db	18538	CTTGCAATTTCCCGAGCTGGGTGTCCGGTGTGACACAGTGCATAATGTGGCGCTTCC	18597	QY	20019	GAATAGATATGCTTGTTCCTTTTAAAAAATGTCACAAATGCAATTTATGATGCTGTGTA	20078
QY	18940	TGTTGCAAACTGCTCACTTAGCTCCGCTTGTGTCGACAGAGAAAGAAATCGAA	18999	Db	19678	GAATAGATATGCTTGTTCCTTTTAAAAAATGTCACAAATGCAATTTATGATGCTGTGTA	19737
Db	18598	TGTTGCAAACTGCTCACTTAGCTCCGCTTGTGTCGACAGAGAAAGAAATCGAA	18657	QY	20079	TAGTAACCTCACAGATCATGCTCCATGAAATGCTTCAGAACCCAAATTAAGGAGATTTT	20138
QY	19000	AATGTTTGGATTTCAAAGTAAACAAGAAGCTGAAAACAACTACTGCGCCAGTCTGAGAG	19059	Db	19738	TAGTAACCTCACAGATCATGCTCCATGAAATGCTTCAGAACCCAAATTAAGGAGATTTT	19797
Db	18658	AATGTTTGGATTTCAAAGTAAACAAGAAGCTGAAAACAACTACTGCGCCAGTCTGAGAG	18717	QY	20139	TAGCCATGTGTGACAAAAGAGAGGCCATTTTCAGTGTGAAATGTTTCAGAGAAATTTG	20198
QY	19060	TTTCAGGGAGACTGCTGAGCCTTGTGTTTTCACCTGACAGCTGAAATGAGCCGACG	19119	Db	19798	TAGCCATGTGTGACAAAAGAGAGGCCATTTTCAGTGTGAAATGTTTCAGAGAAATTTG	19857
Db	18718	TTTCAGGGAGACTGCTGAGCCTTGTGTTTTCACCTGACAGCTGAAATGAGCCGACG	18777	QY	20199	ATTATGTTTCTCAGATCTTTTATTTATTTTGTGAAACAGAGCTCACATTTGCA	20258
QY	19120	TTTCAGGCAAGCTTGTTCCTTCCCTCCTCAAGGTTTACCACAAATCTCAGTTCCTCAGG	19179	Db	19858	ATTATGTTTCTCAGATCTTTTATTTTGTGAAACAGAGCTCACATTTGCA	19917
Db	18778	TTTCAGGCAAGCTTGTTCCTTCCCTCCTCAAGGTTTACCACAAATCTCAGTTCCTCAGG	18837	QY	20259	CCGAGGCTGGAGTACAGTGGCTGGTCTCGGCTCACTGCAACCTCTGCCTCCAGGTC	20318
QY	19180	AAAGCCAAAATTAATTTAGGGTTAGGATTTGGTGTCTTTTATCTAATTCAGGATG	19239	Db	19918	CCGAGGCTGGAGTACAGTGGCTGGTCTCGGCTCACTGCAACCTCTGCCTCCAGGTC	19977
Db	18838	AAAGCCAAAATTAATTTAGGGTTAGGATTTGGTGTCTTTTATCTAATTCAGGATG	18897	QY	20319	AAGGATTTCTCCTGCTGAGCTCCGGAATGCTGGGATTCAGGGCGATGCACCACTGC	20378
QY	19240	ATAATATGTTCTCCACAGATCTTCTGCTGTGTAACAATCTCAGTTCCTGACACTG	19299	Db	19978	AAGGATTTCTCCTGCTGAGCTCCGGAATGCTGGGATTCAGGGCGATGCACCACTGC	20037
Db	18898	ATAATATGTTCTCCACAGATCTTCTGCTGTGTAACAATCTCAGTTCCTGACACTG	18957	QY	20379	CTAATTTTGTATTTTAGTAGAGACAGAGTTTCGCCATGTTGACCAGGCTGCTTCAA	20438
QY	19300	CATATCGAGGATGTTTACTACCAAGGTAAACACAGAAATTTGGTCCCAATTTCCAAATCCC	19359	Db	20038	CTAATTTTGTATTTTAGTAGAGACAGAGTTTCGCCATGTTGACCAGGCTGCTTCAA	20097
Db	18958	CATATCGAGGATGTTTACTACCAAGGTAAACACAGAAATTTGGTCCCAATTTCCAAATCCC	19017	QY	20439	CTCCTGACTTCAGGTGATCCACCACCTCAGCTCCCAAGCACTGGGATTCAGGCGATG	20498
QY	19360	TGAACCTGAGTGAGAGAAATCAGAAATTAATAGGGGATTCACACAGAGCTGGCTACGATG	19419	Db	20098	CTCCTGACTTCAGGTGATCCACCACCTCAGCTCCCAAGCACTGGGATTCAGGCGATG	20157
Db	19018	TGAACCTGAGTGAGAGAAATCAGAAATTAATAGGGGATTCACACAGAGCTGGCTACGATG	19077	QY	20499	AGCCACCGTGCACGCTGTTTCTCAGATCCCTGTA-TTTGTTTCTGAAGCTTCATTTTC	20557
QY	19420	TGCCAGTGGTTCAGATACTTTGCTCATCATACGAGGTGCTGCTGTAGCAACTGCTCA	19479	Db	20158	AGCCACCGTGCACGCTGTTTCTCAGATCCCTGTA-TTTGTTTCTGAAGCTTCATTTTC	20217
Db	19078	TGCCAGTGGTTCAGATACTTTGCTCATCATACGAGGTGCTGCTGTAGCAACTGCTCA	19137	QY	20558	TATCTTCTTATTCATTTTGAAGTAGTACACCTTAAGTAAGGTTTTTAAACAATCAAAATATC	20617
QY	19480	CTGCTTCATTTCTGCTGCTTTTAAATACTGCTTTTCTCAGCTCAATTTGGCTTTCTT	19539	Db	20218	TATCTTCTTATTCATTTTGAAGTAGTACACCTTAAGTAAGGTTTTTAAACAATCAAAATATC	20277
Db	19138	CTGCTTCATTTCTGCTGCTTTTAAATACTGCTTTTCTCAGCTCAATTTGGCTTTCTT	19197	QY	20618	TTTGGAAAAATTCCTGCTGCTTCTTTTATTCCTACAAAAATATGTTTCAGTATAGCTCATG	20677
QY	19540	CCCTCTGGCAGTCACTGTTTCTTGGGTCAACAGCAAAATGATTTCTTTAGAAATCACTGCT	19599	Db	20278	TTTGGAAAAATTCCTGCTGCTTCTTTTATTCCTACAAAAATATGTTTCAGTATAGCTCATG	20337
Db	19198	CCCTCTGGCAGTCACTGTTTCTTGGGTCAACAGCAAAATGATTTCTTTAGAAATCACTGCT	19257	QY	20678	TTTGGAAAAATTCCTGCTGCTTCTTTTATTCCTACAAAAATATGTTTCAGTATAGCTCATG	20737
QY	19600	ACTCAAGGAGCTPACAAAGACATTTGGGATCCACTTCCACTCTCTTTGGAAAAACAATTTTA	19659	Db	20338	TTATGTTTCTTTCAAAATATTCATTTCTCTATCTCAGAAATTTATCTCATGCCCTAAATGTT	20397
Db	19258	ACTCAAGGAGCTPACAAAGACATTTGGGATCCACTTCCACTCTCTTTGGAAAAACAATTTTA	19317	QY	20738	TTATGTTTCTTTCAAAATATTCATTTCTCTATCTCAGAAATTTATCTCATGCCCTAAATGTT	20797
QY	19660	TGGAAGCCAGGTTGCCATAGTGCCTTTGAGGTTGTTTGTCTCAGGAGGCCCAAGCTT	19719	Db	20398	ATTGAATAGTCTTCACATTTCTGTCATCCAGTTTCTGGTCTCTTATTTCACTCTTAAGTCTA	20457
Db	19318	TGGAAGCCAGGTTGCCATAGTGCCTTTGAGGTTGTTTGTCTCAGGAGGCCCAAGCTT	19377	QY	20798	AGTGGCTATTAGATAAAGAGCTTGTAAACAGATTTCTTTCTCCAAATATGCTTATCTTTTG	20857
QY	19720	TGTGCTTCAACATGAATTTAGAGCTTTCAGAAACAAGATCCACATTTTCAATGGCCTCA	19779	Db	20458	ATTGGCTATTAGATAAAGAGCTTGTAAACAGATTTCTTTCTCCAAATATGCTTATCTTTTG	20517
Db	19378	TGTGCTTCAACATGAATTTAGAGCTTTCAGAAACAAGATCCACATTTTCAATGGCCTCA	19437	QY	20858	ACTGCATGCCAGTGACAAAATGTTAACTGTTTGAATCTTCTTCAATTAACATTCACAGAACAT	20917
QY	19780	CCCACTGGATATAAGAACAAATGGCATATCTCAATGACCACCTTTT-TCAGGTGGGATG	19838				

Qy	23078	CAACCTTTGCTCTCCCGGGCTCAGCGAATTTCTCCACCTCAGCCTCCCGAGCAGCTGAAC	23133
Db	22738	CAACCTTTGCTCTCCCGGGCTCAGCGAATTTCTCCACCTCAGCCTCCCGAGCAGCTGAAC	22797
Qy	23138	ACAGCGCTGTGCCACCACTCCCGCAATTTTTTTTTTCCATTTTGTAGTAAATGGGGTTT	23197
Db	22798	ACAGCGCTGTGCCACCACTCCCGCAATTTTTTTTTTCCATTTTGTAGTAAATGGGGTTT	22857
Qy	23198	CACCATGTTGCCTGGGCTGTCTTGAACTCCTGGGCTCAGGCAATCCACCGCCTTGCC	23257
Db	22858	CACCATGTTGCCTGGGCTGTCTTGAACTCCTGGGCTCAGGCAATCCACCGCCTTGCC	22917
Qy	23258	TCCCAAAAGTCTAGCATTTACAGSCATAGCCACCGCGCTGCACCTCAATTTCTTAGACT	23317
Db	22918	TCCCAAAAGTCTAGCATTTACAGSCATAGCCACCGCGCTGCACCTCAATTTCTTAGACT	22977
Qy	23318	AAATAAATCGAGATGGCTAAAGATTTCTATGTAGGCCAACTATGTTTTTAAAG-TT	23376
Db	22978	AAATAAATCGAGATGGCTAAAGATTTCTATGTAGGCCAACTATGTTTTTAAAGTTT	23037
Qy	23377	TTTTTTTTAAGGATATCTGCTGAAACCAATCATGCCCACCAACCAAGATGCAAGCACTATA	23436
Db	23038	TTTTTTTTAAGGATATCTGCTGAAACCAATCATGCCCACCAACCAAGATGCAAGCACTATA	23097
Qy	23437	AAACATACCAGTTTTTCAAAGCATTTAAAAATTTCTCTAAAAATATTTTTTCTCCAGAA	23496
Db	23098	AAACATACCAGTTTTTCAAAGCATTTAAAAATTTCTCTAAAAATATTTTTTCTCCAGAA	23157
Qy	23497	ATTTTGATTTGATTCCTGAGAGCAATTAATATGGGACCTGACCTATAAATGATGAAC	23556
Db	23158	ATTTTGATTTGATTCCTGAGAGCAATTAATATGGGACCTGACCTATAAATGATGAAC	23217
Qy	23557	TCAATCTCCCACTCAAGGTAGGAGTCTCTCAGATTTAAAAATTAAGCATCTCTAGTCCTC	23616
Db	23218	TCAATCTCCCACTCAAGGTAGGAGTCTCTCAGATTTAAAAATTAAGCATCTCTAGTCCTC	23277
Qy	23617	TTGTCCCTGTAAAGTTAACCTTTACCTCGAAACACAGGAGACTGCGGTTGTTGCA	23676
Db	23278	TTGTCCCTGTAAAGTTAACCTTTACCTCGAAACACAGGAGACTGCGGTTGTTGCA	23337
Qy	23677	TAGGGTTCAATTTAAAGTTGAGTCACTCCTGACATCTATTAAACCAACCAATTTAGTAAAC	23736
Db	23338	TAGGGTTCAATTTAAAGTTGAGTCACTCCTGACATCTATTAAACCAACCAATTTAGTAAAC	23397
Qy	23737	TATGCATGTATGAGACTTTTATGATTTGAACCTGTTTTATGAGTCAAGAGATATAGTTTA	23796
Db	23398	TATGCATGTATGAGACTTTTATGATTTGAACCTGTTTTATGAGTCAAGAGATATAGTTTA	23457
Qy	23797	CAATGAAATTTGGGCAATCAAAATGACCTTGCTTAGCTTAGCATTTGCTCATGTTA	23856
Db	23458	CAATGAAATTTGGGCAATCAAAATGACCTTGCTTAGCTTAGCATTTGCTCATGTTA	23517
Qy	23857	ACTATTTCTTCATTTGGGCTGATTTTAGTTGCTTTAGGAAAAATCAAAACACACACTTT	23916
Db	23518	ACTATTTCTTCATTTGGGCTGATTTTAGTTGCTTTAGGAAAAATCAAAACACACACTTT	23577
Qy	23917	AAAATTTATTAATAATCCCGTCTTAACCTCAGAGTCAGAACCGCATCTCTAAACCTGGT	23976
Db	23578	AAAATTTATTAATAATCCCGTCTTAACCTCAGAGTCAGAACCGCATCTCTAAACCTGGT	23637
Qy	23977	CATGCATAATATGTTTAAATTTTTTGTGCTTTTAAAACTACAAATTAAGGAATGTTTAATA	24036
Db	23638	CATGCATAATATGTTTAAATTTTTTGTGCTTTTAAAACTACAAATTAAGGAATGTTTAATA	23697
Qy	24037	GTTCCCAATTCATATGTCATGTTAGCCGAGGGAAGATTAGCATAGTTTAAAGACTTAAATG	24096
Db	23698	GTTCCCAATTCATATGTCATGTTAGCCGAGGGAAGATTAGCATAGTTTAAAGACTTAAATG	23757
Qy	24097	GCTTTTCAACATATATCAAAAGCAAAAAATTAAGGGGAACAGAGTCTAGAAATGAGGAAC	24156
Db	23758	GCTTTACACATATATCAAAAGCAAAAAATTAAGGGGAACAGAGTCTAGAAATGAGGAAC	23817
Qy	24157	TGGGACACAGGCAAAAAAATAATTAAGAACTCGGCATGTAATACCGCAAGGGATAAGAC	24216

Db	23818	TTGGGACACAGGCAAAAAAATAAGAGAACTGGGACATGAATTAACGCAAGGGAATAGAC	23877
Qy	24217	TAAATACAAAAACACCCCAATAATAATAGCAGCATTTGCTGAGCTCTTACTGTGAGCCTG	24276
Db	23878	TAAATACAAAAACACCCCAATAATAATAGCAGCATTTGCTGAGCTCTTACTGTGAGCCTG	23937
Qy	24277	TTCTAAGCAGCTTTACATATATTAACCTCAITTTCACTCTCAAGGAACCATCTGAGGCAGGCA	24336
Db	23938	TTCTAAGCAGCTTTACATATATTAACCTCAITTTCACTCTCAAGGAACCATCTGAGGCAGGCA	23997
Qy	24337	CTGTTATCATCTCCATTTTACAGATAAAGNATAGACCCAGAGAGGCTGAGCAACTTGGGCC	24396
Db	23998	CTGTTATCATCTCCATTTTACAGATAAAGNATAGACCCAGAGAGGCTGAGCAACTTGGGCC	24057
Qy	24397	TATTTCCACAGCTACTATGGTGGAGATTCAGATTTAAATCTAAATCATTTGGCTCCAGAGCCCA	24456
Db	24058	TATTTCCACAGCTACTATGGTGGAGATTCAGATTTAAATCTAAATCATTTGGCTCCAGAGCCCA	24117
Qy	24457	TGGACCCAAATGGCTGCATCAAGTGAATGATCGATCGGCTATCAACGTTGCCAAAGTGGGCCA	24516
Db	24118	TGGACCCAAATGGCTGCATCAAGTGAATGATCGATCGGCTATCAACGTTGCCAAAGTGGGCCA	24177
Qy	24517	CAGCTCGGATCTCGGTTTTCCAGTAGCCAAAGCAGAGAGTGTAATCAGACCTCACTTTAA	24576
Db	24178	CAGCTCGGATCTCGGTTTTCCAGTAGCCAAAGCAGAGAGTGTAATCAGACCTCACTTTAA	24237
Qy	24577	TAAACAGTCTCAAGCCAGAGAGAGTGGTATTCAGGCAGCAACAGGCTGCTAGTCGAAA	24636
Db	24238	TAAACAGTCTCAAGCCAGAGAGAGTGGTATTCAGGCAGCAACAGGCTGCTAGTCGAAA	24297
Qy	24637	TCCCACTTCTCTCTCAGTGGTCCATACAGTTTTACTCTACTTGTCTTACAGATCAAAAT	24696
Db	24298	TCCCACTTCTCTCTCAGTGGTCCATACAGTTTTACTCTACTTGTCTTACAGATCAAAAT	24357
Qy	24697	AGCTGGAGTTTCAGTGGCGTTTCAATGCCCTGTGTGAGAGTTGGCTTTTCAAGTTTAT	24756
Db	24358	AGCTGGAGTTTCAGTGGCGTTTCAATGCCCTGTGTGAGAGTTGGCTTTTCAAGTTTAT	24417
Qy	24757	TTTTTGTGTGTTTTTAAATAGACTCTACTTTTTTAAAGAAATTTTGTAGATTTTACAGAGA	24816
Db	24418	TTTTTGTGTGTTTTTAAATAGACTCTACTTTTTTAAAGAAATTTTGTAGATTTTACAGAGA	24477
Qy	24817	TTGAGAGGATGATACAGAGATTCGCGTATACCTCACCCAGTTTCTGCAATTTAATAC	24876
Db	24478	TTGAGAGGATGATACAGAGATTCGCGTATACCTCACCCAGTTTCTGCAATTTAATAC	24537
Qy	24877	CTCTTACATTCATGCGGTACATTTGTATCAATTAATGACGAGCGCGCGCGGCACAGT	24936
Db	24538	CTCTTACATTCATGCGGTACATTTGTATCAATTAATGACGAGCGCGCGCGGCACAGT	24597
Qy	24937	GGTTTCAGGCCCCCTAAATCCAGACACTTTGGGAGGACAGAGCAAGCAATCACTTGAGGTCA	24996
Db	24598	GGTTTCAGGCCCCCTAAATCCAGACACTTTGGGAGGACAGAGCAAGCAATCACTTGAGGTCA	24657
Qy	24997	GGAGTTTCGAGACTAGCCTGACCAACATGTGTAAACCCCTTTCTGTACTAAAAATACAAAAA	25056
Db	24658	GGAGTTTCGAGACTAGCCTGACCAACATGTGTAAACCCCTTTCTGTACTAAAAATACAAAAA	24717
Qy	25057	TTAGCCAGGCATCGTCTGGTTGCCGTATTTCCACAGATACTCAGGAGGCTGAGGCACAAG	25116
Db	24718	TTAGCCAGGCATCGTCTGGTTGCCGTATTTCCACAGTACTCAGGAGGCTGAGGCACAAG	24777
Qy	25117	AATTTGTTGAACAGGGAGGGGAGGTTGCATGAAGCGGAGATCTGTGCCACTGCCA	25176
Db	24778	AATTTGTTGAACAGGGAGGGGAGGTTGCATGAAGCGGAGATCTGTGCCACTGCCA	24837
Qy	25177	GCCTGGGCAACAGAGCGAGACTCCATCAAAAAAATAAAAAAATAAAAAAAGAGGAAGAA	25236
Db	24838	GCCTGGGCAACAGAGCGAGACTCCATCAAAAAAATAAAAAAATAAAAAAAGAGGAAGAA	24897
Qy	25237	GGAGGAAAAATTAAATGAGCCCAATATTGAGACATTTATTACTAAAGTCCATGCTTATG	25296

QY	31824	GTCTTTGGGAGACAGTTTTTCCATGACCACTGCTCAGGGGCTGGGAGGCATGCTTTTG	31883	Db	32572	ACCTTATTATGTAACCTTAAGCTAGGATCATAGATCCCTACTTGTCTCGTGTCTTTATAA	32631
Db	31494	GTCTTTGGGAGACAAATTTTCCATGACCACTGCTCAGGGGCTGGGAGGCATGCTTTTG	31553	QY	32961	AGCAGACAAACACC--GGGAAATCATTATTAAGACAGGAAAGGCCAAGTGCAGTGGCTC	33018
QY	31884	GGATGAGTCAAGTACATACCTTTGTTGTATACCTTTATTTCTATTATTAATTATGTA	31943	Db	32632	GCCAGACAAACACC--GGGAAATCATTATTAAGACAGGAAAGGCCAAGTGCAGTGGCTC	32691
Db	31554	GGATGAGTCAAGTACATACCTTTGTTGTATACCTTTATTTCTATTATTAATTATGTA	31613	QY	33019	ATGCGCTTAATCCAGACACTTTGGGAAATTTGAGGGAGTGGATCAACTGAAGTCAAGAG	33078
QY	31944	TATATAATGAATAATTAACACCTCACCATAATGTAGGAATCAGTGGGAGCCCTAAGT	32003	Db	32692	ATGCGCTTAATCCAGACACTTTGGGAAATTTGAGGGAGTGGATC--ACCTGAAGTCAAGAG	32750
Db	31614	TATATAATGAATAATTAACACCTCACCATAATGTAGGAATCAGTGGGAGCCCTAAGT	31671	QY	33079	TTTGAGACCAAACTCACCAGCATGACAGAACCCCATCTCTACTAAAAATACAAAAATTAG	33138
QY	32004	TTGTTTTCTGCAACTAGACAGTCCCATCTGGGGGCAATGGGAGATAGTACAGATCATC	32063	Db	32751	TTTGAGACCAAACTCACCAGCATGACAGAACCCCATCTCTACTAAAAATACAAAAATTAG	32810
Db	31672	TTGTTTTCTGCAACTAGACAGTCCCATCTGGGGGCAATGGGAGATAGTACAGATCATC	31731	QY	33139	TTGGGCATGGTGCATGTGCTCTCTCAAAAATTTAATAAAGCTACTCAAAAGCTAGGGCAGGAAAAATC	33198
QY	32064	AAGCATTTAGATTCTCATTAAGAGTGTCTAGCTAGATCCCGGCATGTGAGTTCAAT	32123	Db	32811	TTGGGCATGGTGCATGTGCTCTCTCAAAAATTTAATAAAGCTACTCAAAAGCTAGGGCAGGAAAAATC	32870
Db	31732	AAGCATTTAGATTCTCATTAAGAGTGTCTAGCTAGATCCCGGCATGTGAGTTCAAT	31791	QY	33199	ACTTCAACCGAGGATGCCAAGATAGCAGTGGCCAAATCTGTCACCTGCCTCCAGTCT	33258
QY	32124	AGGATTTGCTCACCTATGAGAACTAATGCACTGTGCTGATCTGACAGGAGTGGAGCTCG	32183	Db	32871	ACTTCAACCGAGGATGCCAAGATAGCAGTGGCCAAATCTGTCACCTGCCTCCAGTCT	32930
Db	31792	AGGATTTGCTCACCTATGAGAACTAATGCACTGTGCTGATCTGACAGGAGTGGAGCTCG	31851	QY	33259	GGATGATAGACCAAGATCCTGCTCAAAAATTTAATAAAGCTACTCAAAAGCTAGGGCAGGAAAAATC	33318
QY	32184	GGGATTAATGCGAGGTTGGGAGCAGCTGTCAATATAGATGAAGCTTTGCTCGCTCGCC	32243	Db	32931	GGATGATAGACCAAGATCCTGCTCAAAAATTTAATAAAGCTACTCAAAAGCTAGGGCAGGAAAAATC	32990
Db	31852	GGGATTAATGCGAGGTTGGGAGCAGCTGTCAATATAGATGAAGCTTTGCTCGCTCGCC	31911	QY	33319	CCTTTTCCAAAGGAGACCTTCTGCTTGTCTAGTTCAGAGAACTTCTCTTTTGGAGAAAAAC	33378
QY	32244	TGCCACTCACTCTCTGCTGTGTGCTCCACTTCTTACAGGTACAGACTGCTACTGGTCC	32303	Db	32991	CCTTTTCCAAAGGAGACCTTCTGCTTGTCTAGTTCAGAGAACTTCTCTCTTTTGGAGAAAAAC	33049
Db	31912	TGCCACTCACTCTCTGCTGTGTGCTCCACTTCTTACAGGTACAGACTGCTACTGGTCC	31971	QY	33379	AAACACCCAGTCCATTAGCAGCAACCTCAGGGATTGAATCTCTAGGGCAGCAGGCTGGGC	33438
QY	32304	ATGCCAGGAGTTGGGACCCCTGTCTTAGGGAGTAGGGGTGGAGTTCCCTTCACTTCTA	32363	Db	33050	AAACACCCAGTCCATTAGCAGCAACCTCAGGGATTGAATCTCTAGGGCAGCAGGCTGGGC	33109
Db	31972	ATGCCAGGAGTTGGGACCCCTGTCTTAGGGAGTAGGGGTGGAGTTCCCTTCACTTCTA	32031	QY	33439	ACAGTGGCTCATGCTGTATCCAGTACTTTGGAGGCTGAGATGGGTGGATCACTTGA	33498
QY	32364	GAAGCCCTGATAGTATCCAGAGCTGTCAATACAGATATCAAAACAGGTTGGCTA	32423	Db	33110	ACAGTGGCTCATGCTGTATCCAGTACTTTGGAGGCTGAGATGGGTGGATCACTTGA	33169
Db	32032	GAAGCCCTGATAGTATCCAGAGCTGTCAATACAGATATCAAAACAGGTTGGCTA	32091	QY	33499	CATCAGGTGTTTCGAGACAGCCTGCGCAACATGTTGAAACTCTCTCTCAAAAAATAT	33558
QY	32424	AAACAGACATGAATCTCTCTTATTTTGTATGGCTTGAAGTCCAAAGTCAAGGTGCTG	32483	Db	33170	CATCAGGTGTTTCGAGACAGCCTGCGCAACATGTTGAAACTCTCTCTCAAAAAATAT	33229
Db	32092	AAACAGACATGAATCTCTCTTATTTTGTATGGCTTGAAGTCCAAAGTCAAGGTGCTG	32151	QY	33559	GAAAAAAGGCTGGGTGTTGGCTTATCGCTGTAGTCTCAGTACC	33618
QY	32484	CCAGGCCATGCTCCCTCTGAATGTGTAGGGAGAACTCTCTTCTCTTCTAGCTT	32543	Db	33230	G--AAAAAAGGCTGGGTGTTGGCTTATCGCTGTAGTCTCAGTACC	33288
Db	32152	CCAGGCCATGCTCCCTCTGAATGTGTAGGGAGAACTCTCTTCTCTTCTAGCTT	32211	QY	33619	TGGGAGGCTGAAGCAGGAGATCACTTGAACCCGGGAGTTGGAGTTGCAGTGGAGTGA	33678
QY	32544	CTGGTGTGTTGGGCAATCACTGGCATCGCTTGGCTTGCAGCACTTCAACATCTGCCTT	32603	Db	33289	TGGGAGGCTGAAGCAGGAGATCACTTGAACCCGGGAGTTGGAGTTGCAGTGGAGTGA	33348
Db	32212	CTGGTGTGTTGGGCAATCACTGGCATCGCTTGGCTTGCAGCACTTCAACATCTGCCTT	32271	QY	33679	ATTGCCCTACTGTACTCCAACTGGGTGACAGAGAGACTCCCATCTCAAAAAATAAAG	33738
QY	32604	TACTGTCTCATAGTGTCTCCCTCATGTCTCCAGGTCTCTCTGTCTCTCTCTTTGTAT	32663	Db	33349	ATTGCCCTACTGTACTCCAACTGGGTGACAGAGAGACTCCCATCTCAAAAAATAAAG	33408
Db	32272	TACTGTCTCATAGTGTCTCCCTCATGTCTCCAGGTCTCTCTGTCTCTCTCTTTGTAT	32331	QY	33739	AATTCCTGGGAGGAGTCTTCTCTCACTCATAGACCATGGAGGTGAGCCAGTCTGA	33798
QY	32664	ARGGAACATGATCATATTTGATTAAGGCCAACCTTACTCTAGTATGACTCATCTTAAG	32723	Db	33409	AATTCCTGGGAGGAGTCTTCTCTCACTCATAGACCATGGAGGTGAGCCAGTCTGA	33468
Db	32332	AAGGAACATGATCATATTTGATTAAGGCCAACCTTACTCTAGTATGACTCATCTTAAG	32391	QY	33799	CAAAACATGAGAAACAAATGGGAGAGACATACCTGTAACTGACTGCTGGGCAAGGACAA	33858
QY	32724	GTCAATGCAATGACTATTCCAGATAAGGTCAATTTCTGAAGAACTGGGAGTTAGGACTT	32783	Db	33469	CAAAACATGAGAAACAAATGGGAGAGACATACCTGTAACTGACTGCTGGGCAAGGACAA	33528
Db	32392	GTCAATGCAATGACTATTCCAGATAAGGTCAATTTCTGAAGAACTGGGAGTTAGGACTT	32451	QY	33859	AGGTGAGAAATGACAAAGTTTGGAGAACTATGAGACAGGAGTGGGGAACACCACTAG	33918
QY	32784	CATATCTTTTGAAGGAACACAGTTTCAACCAATTAAGCCCTGTACTGTTTACAAATAG	32843	Db	33529	AGGTGAGAAATGACAAAGTTTGGAGAACTATGAGACAGGAGTGGGGAACACCACTAG	33588
Db	32452	CATATCTTTTGAAGGAACACAGTTTCAACCAATTAAGCCCTGTACTGTTTACAAATAG	32511	QY	33919	CAGAAATGATGGAAGTTCTCAAGAAATCAACAGAGAAATAGACCATGGCCAGGAGTCTAG	33978
QY	32844	GTATTCCTCTCTCCCTCCCAAGTTCTTATAGCAGACAACTTGTACCAAAAGGCAAAAT	32903	Db	33589	CAGAAATGATGGAAGTTCTTCAAGAAATCAACAGAGAAATAGACCATGGCCAGGAGTCTAG	33648
Db	32512	GTATTCCTCTCTCCCTCCCAAGTTCTTATAGCAGACAACTTGTACCAAAAGGCAAAAT	32571	QY	33979	AACCTCTCAGGAAAGGAGATGGGCTCCAGGAGCAGAGGAGGAGCTTCAAGGGGAATGGG	34038
QY	32904	ACCTTATTATGTAACCTTAACCTPAGGATCATAGATCCCTAC--TGCTGTGTGCTTT--ATA	32960				

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Db 33709 AGTGGGTGAATATATAGACGATGGGGAACAACCAAGACGATCGCTATTGCAAACTGA 33768
Qy 34099 GGAGAGGAGAGCTCGAGGGGGTGGTGGGAAGCTGGGCTCCTTAAGGAGGTTTGAACA 34158
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Qy 34159 AAGCAGTCATGGAGCGGGCTTGAATACAGTGGGGAAGGTTAAAGTTCTCTCGGAT 34218
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QY 37216 CTTATCATCTTTGAAGTTTATGTCATGGGCTGACTTCAAACTCAACTTTAAATTTATAT 37275
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SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1		
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TITLE	A novel nucleic acid molecule		
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	DESIRE DU (AU) ; AMRAD OPERATIONS PTY LTD (AU)		
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DB	2	GTTTGAATTTGTTNATAAGGAAGTTTGAATCAATCCGGAAGAAATTTTTTTTTTAAAAA	61
QY	352	ATTTTCTGAATGTCTGTATTAACATAGCCACTTCGCTTTTAAATTAGTATTTT	411
DB	62	ATTTTCTGAAGG-GTTTGTATTAATAAACCAATTTGGTTTTTAAATAGGATTT	120

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Db	13370	GAATTTCAATGCTGTTTTTAAACCATCTAGGAAATGTTGATTTCTAATGAAAATTTACTGC	13429	QY	14777	TCTGTGCAAGGAGCAATATGGTAGAATTTCTAATATTCAGGCAG-ACAAACATTTCTCTG	14835
QY	13710	TGAAAATGGGCTGAAAATGCTGGGCTGGAATATTTGTTATTAATCTTACATGATTTCCAGT	13769	Db	14509	TCTGTGCAAGGAGCAATATGGTAGAATTTCTAATATTCAGGCAGTACACATTTCTCTG	14568
Db	13430	TGAAAATGGGCTGAAAATGCTGGGCTGGAATATTTGTTATTAATCTTACATGATTTCCAGT	13489	QY	14836	CATTTGTAGCAGGTAAAGGAGGTTCAGGCAGAAAGACAAACCACTGGGAGCTGCACAAAG	14895
QY	13770	GTTGTATTAATATTTTCTTTTCTTTTGTGACCCGATATAGATGAAGCAAGAGACA	13829	Db	14569	CATTTGTAGCAGGTAAAGGAGGTTCAGGCAGAAAGACAAACCACTGGGAGCTGCACAAAG	14628
Db	13490	GTTGTATTAATATTTTCTTTTCTTTTGTGACCCGATATAGATGAAGCAAGAGACA	13549	QY	14896	GGCATAAACGCTAATGCACCTGATGTAGTGTAAATTTGTTATTCAGCTAAAGATCT	14955
QY	13830	A-GGACCAATCCCATGCTGAATAGAAAAGGAGCGCTGAATTTGTTGCTGTTTTTGA	13888	Db	14629	GGCATAAACGCTAATGCACCTGATGTAGTGTAAATTTGTTATTCAGCTAAAGATCT	14688
Db	13550	AGGAGCAATCCCATGCTGAATAGAAAAGGAGCGCTGAATTTGTTGCTGTTTTTGA	13609	QY	14956	TTCTAATAAATAAACTTATCATTTGTAGGAGGCAAGAAATCGTGGAAAGCTGGGATT	15015
QY	13889	ATTTAAGCTGGTTTTCCGATTAAATTCAGTAAATGGTCCAGGACTATAAATGTTGAACATT	13948	Db	14689	TTCTAATAAATAAACTTATCATTTGTAGGAGGCAAGAAATCGTGGAAAGCTGGGATT	14748
Db	13610	ATTTAAGCTGGTTTTCCGATTAAATTCAGTAAATGGTCCAGGACTATAAATGTTGAACATT	13669	QY	15016	CAGGTTGCCCTGCTGCTTTAATCTGGAATCAGAAATATTAGTCAAGGATATCAGCTATG	15075
QY	13949	TTTTACCGTGAATTTAAATTTAGTCTTAATGT-----TTTTTTTTTTTTTTG	13996	Db	14749	CAGGTTGCCCTGCTGCTTTAATCTGGAATCAGAAATATTAGTCAAGGATATCAGCTATG	14808
Db	13670	TTTTACCGTGAATTTAAATTTAGTCTTAATGTTTTTTTTTTTTTTTTTTTTTTTG	13729	QY	15076	AAGTAAGTTTTCAATGTTATATGCAAGATGCAGCTGCTCTTATTTTCACTTCCAGTAA	15135
QY	13997	ATGTTTTACATTTTCCCATGGGAAGCAGCTATGTCATGTCGGCATGATTTCATCATGTA	14056	Db	14809	AAGTAAGTTTTCAATGTTATATGCAAGATGCAGCTGCTCTTATTTTCACTTCCAGTAA	14868
Db	13730	ATGTTTTACATTTTCCCATGGGAAGCAGCTATGTCATGTCGGCATGATTTCATCATGTA	13789	QY	15136	TTCTTCTGAAATTAATACACCTTAAATAAGTGCAGCTTCTTAAATCTGTGAGAAATCGT	15195
QY	14057	ACATCTCGGGTATTTTGGTTGTGTATGTTTCAAGAAAGCGAATGCCAAAATAAAGAG	14116	Db	14869	TTCTTCTGAAATTAATACACCTTAAATAAGTGCAGCTTCTTAAATCTGTGAGAAATCGT	14928
Db	13790	ACATCTCGGGTATTTTGGTTGTGTATGTTTCAAGAAAGCGAATGCCAAAATAAAGAG	13849	QY	15196	ATGTGCTGCTGTGCACACTTTC--TTTTTCTGTAAGGCTCTTTGAGGCTTTTCAAGAACT	15253
QY	14117	TGGTTTGTGATGCTAGTGTCTCTTCTTACAAATCAAGCTTTTATTTTAAATCCACT	14176	Db	14929	ATGTGCTGCTGTGCACACTTTC--TTTTTCTGTAAGGCTCTTTGAGGCTTTTCAAGAACT	14988
Db	13850	TGGTTTGTGATGCTAGTGTCTCTTCTTACAAATCAAGCTTTTATTTTAAATCCACT	13909	QY	15254	CAATTTCAATTCAGCAACAAATTAGGGGTCTAAGGTATACAGACCTGTGCAAGATGCTCC	15313
QY	14177	TAAATGGGCACTGCAGAAATTTAAAAAATGGAAGTCCCATCCACAGAAAGCGAGTACTAT	14236	Db	14989	CAATTTCAATTCAGCAACAAATTAGGGGTCTAAGGTATACAGACCTGTGCAAGATGCTCC	15048
Db	13910	TAAATGGGCACTGCAGAAATTTAAAAAATGGAAGTCCCATCCACAGAAAGCGAGTACTAT	13969	QY	15314	TGAGACACAAAGAGGAGTCAAGCCCTGCTTCAGGCACCTCTCTATATATAGGAGGA	15373
QY	14237	GATGTAAGAAAGTTAGTGGGGATTAATAGAGTGATCATATAATTTATGAGCTAAACCG	14296	Db	15049	TGAGACACAAAGAGGAGTCAAGCCCTGCTTCAGGCACCTCTCTATATATAGGAGGA	15108
Db	13970	GATGTAAGAAAGTTAGTGGGGATTAATAGAGTGATCATATAATTTATGAGCTAAACCG	14029	QY	15374	GAAGAAGAAACACATAACATAGGTAGGTGCCATTAAGAGGGGTACATACATTAAA	15433
QY	14297	GAGGCACTTTTTTTTGTAGATCGAGTCTCACCTGTTTGCCTAGGCTGGAGTGCAGTGACGT	14356	Db	15109	GAAGAAGAAACACATAACATAGGTAGGTGCCATTAAGAGGGGTGCATACATTAAA	15168
Db	14030	GAGGCACTTTTTTTTGTAGATCGAGTCTCACCTGTTTGCCTAGGCTGGAGTGCAGTGACGT	14089	QY	15434	GCCAGGTGTTAGGTGAAGAGATTTTGAACATGAGAAATTTTCTGCATGTTTGAATATC	15493
QY	14357	GATCAGAGCTCACTGCAACCTCCGCTCCGGGTTCAAGGATTTCTCATGCTCAGCCTC	14416	Db	15169	GCCAGGTGTTAGGTGAAGAGATTTTGAACATGAGAAATTTTCTGCATGTTTGAATATC	15228
Db	14090	GATCAGAGCTCACTGCAACCTCCGCTCCGGGTTCAAGGATTTCTCATGCTCAGCCTC	14149	QY	15494	TTATAATTTTAAAAATTTAAAAATGGGAGATACATATATGTTATTTATGTTGTTATAT	15553
QY	14417	CTGAGTAGCTGGAGCTATAGCGCCCAACCATGCCAGCTAACGTTATTTTGTGTTTTTGT	14476	Db	15229	TTATAATTTTAAAAATTTAAAAATGGGAGATACATATATGTTATTTATGTTGTTATAT	15288
Db	14150	CTGAGTAGCTGGAGCTATAGCGCCCAACCATGCCAGCTAACGTTATTTTGTGTTTTTGT	14209	QY	15554	GTATGTACATATACACATATATACATAAATATATACATAAATATGTTATATGTTGTTAT	15613
QY	14477	AGAGATGGGGTTTTTACCATGTTGGCCAGGCTTCTTCAAACTCCTGACCTCAGGTGATCC	14536	Db	15289	GTATGTACATATACACATATATACATAAATATATACATAAATATGTTATATGTTGTTAT	15348
Db	14210	AGAGATGGGGTTTTTACCATGTTGGCCAGGCTTCTTCAAACTCCTGACCTCAGGTGATCC	14269	QY	15614	ATAGCATATAATATGTTATATGTTATATACATAAATATGTTATATGTTGTTATATAG	15673
QY	14537	GCCCACTCGACCTCTAACTGCTGGATTACAGCGGTAAAGCACCATGCTGCGCCAG	14596	Db	15349	ATAGCATATAATATGTTATATGTTATATACATAAATATGTTATATGTTGTTATATAG	15408
Db	14270	GCCCACTCGACCTCTAACTGCTGGATTACAGCGGTAAAGCACCATGCTGCGCCAG	14329	QY	15674	ACATAAATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATAGACAT	15733
QY	14597	AGACACTTTTGTAGAGTGAAGAGGAAGCTGAGAATAATTCATCTACAACTGGGACCA	14656				

Db	15409	ACATAAATATGTATATATGTATATATAGACATAAAATATGTATATATGTATATGTATATAGACAT	15466
Qy	15734	AAATATGTATATATGTGTATATAGACATAAAATATGTATATATATGTGTATATAGACATAAAT	15793
Db	15469	AAATATG--TATATGTGTATATAGACATAAAATATGTATATATGTGTATATAGACATAAAT	15526
Qy	15794	ATGTATATATGTGTATATAGACATAAAATATGTATATATGTGTATATAGACATAAAATATGT	15853
Db	15527	ATGTATATATGTGTATATAGACATAAAATATGTATATATGTGTATATAGACATAAAATATGT	15586
Qy	15854	ATATATGTGTATATAGACATAAAATATGTATATATGTGTATATAGACATAAAATATGTATAT	15913
Db	15587	ATATATGTGTATATAGACATAAAATATGTATATATGTGTATATAGACATAAAATATGTATAT	15646
Qy	15914	ATGTGTATATAGACATAAAATATGTATATATGTGTATATAGACATAAAATATGTATATATGT	15973
Db	15647	ATGTGTATATAGACATAAAATATGTATATATGTGTATATAGACATAAAATATGTATATATGT	15706
Qy	15974	GTATATAGACATAAAATATGTATATATGTGTATATAGACATAAAATATGTATATATGT--NGT	16032
Db	15707	GTATATAGACATAAAATATGTATATGTGTGTATATAGACATAAAATATGTATATATGTGTGT	15766
Qy	16033	ATATAGACATAAAATATGTATATGTGTGTATATATATATATGTGTGT--CATATACACAT	16091
Db	15767	ATATAGACATAAAATATGTATATGTGTGTATATATATATATGTGTATATATACACAT	15926
Qy	16092	ATATACATACATAAAACATTTCTGCATTATACCATTCACITTTGTAACCCCATCTTCCCTAAAA	16151
Db	15827	ATATACATACATAAAACATTTCTGCATTATACCATTCACITTTGTAACCCCATCTTCCCTAAAA	15886
Qy	16152	ACTGTCTCAATAAGAGTCCTTTTCCCTGTACCTATGCAATGGTAAGTAGCAAAACACA	16211
Db	15987	ACTGTCTCATAAAGAGTCCTTTTCCCTGTACCTATGCAATGGTAAGTAGCAAAACACA	15946
Qy	16212	CATTCTTTTGGGTCCCAATAACAATCCCTGTAGTTTGGCCCTTAAACAGTCCTTTGATGTGAA	16271
Db	15947	CATTCTTTTGGGTCCCAATAACAATCCCTGTAGTTTGGCCCTTAAACAGTCCTTTGATGTGAA	16006
Qy	16272	ATTATCTGTTTCGTCTTAACCTTGCTGCTGCGGTACATGAGAGTTTTGGCTCCTGGCT	16331
Db	16007	ATTATCTGTTTCGTCTTAACCTTGCTGCTGCGGTACATGAGAGTTTTGGCTCCTGGCT	16066
Qy	16332	CCTAGTCTGCATCTTCAACCCCATCCCTTCCCAAAAGAAATCTGGTTATGTGACCACTGCTC	16391
Db	16067	CCTAGTCTGCATCTTCAACCCCATCCCTTCCCAAAAGAAATCTGGTTATGTGACCACTGCTC	16126
Qy	16392	ATCTTTTCTGCTGCCCAACTCCAGTCCCAAGCCACAAACCTCTCTCTCTGGACTCCTGC	16451
Db	16127	ATCTTTTCTGCTGCCCAACTCCAGTCCCAAGCCACAAACCTCTCTCTCTGGACTCCTGC	16186
Qy	16452	GGGAGATTCCTTCTCTCCCTGCATGAGTCTATTTCTCCGCACAACTGGCATAGGTAAGTG	16511
Db	16187	GGGAGATTCCTTCTCTCCCTGCATGAGTCTATTTCTCCGCACAACTGGCATAGGTAAGTG	16246
Qy	16512	AGACTCGGAAGAGGCAAGTTTGCAGAGTCCAGAGGAAATGAAGACTCTGCTTGTGCACAT	16571
Db	16247	AGACTCGGAAGAGGCAAGTTTGCAGAGTCCAGAGGAAATGAAGACTCTGCTTGTGCACAT	16306
Qy	16572	GCTGGGTTTCAAGGGTGTGGATATCCGATGGATGGCCCTTAAAGTGTAGCTCAAGGCTTA	16631
Db	16307	GCTGGGTTTCAAGGGTGTGGATATCCGATGGATGGCCCTTAAAGTGTAGCTCAAGGCTTA	16366
Qy	16632	AGGAGAGATAGGGGTGTAGTACTCAGATTCATCAGTGTGGCTGATGTTTAAACCCA	16691
Db	16367	AGGAGAGATAGGGGTGTAGTACTCAGATTCATCAGTGTGGCTGATGTTTAAACCCA	16426
Qy	16692	GGGACAGGATAGAAGGTTATTCCAGGAGAGCGTGTAGATAAAGAGCTTAATGCTTCT	16751
Db	16427	GGGACAGGATAGAAGGTTATTCCAGGAGAGCGTGTAGATAAAGAGCTTAATGCTTCT	16486
Qy	16752	GGGTCTTTAGTCATTCAAATCGGACCTCTGAGGACGAGGAAAGCCCAAGAGTAGA	16811
Db	16487	GGGTCTTTAGTCATTCAAATCGGACCTCTGAGGACGAGGAAAGCCCAAGAGTAGA	16546

QY	17892	AAAAAGAGAAAGAAAGAAAGAAATACCTCCAGAGAGCCAGGTCCTCTTAGGCGCTTCT	Db	18707	GCTGGCAGCAGAGAAAGAAAGAAATCGAATGTTGGATTTCAAGGTACAGAGACT	17951
Db	17627	AAAAAGAGAAAGAAAGAAAGAAATACCTCCAGAGAGCCAGGTCCTTAGGCGCTTCT	QY	19031	GGAAAAACAATCTAGTGGCCGAGCTGTAGAGTTTTCAGCGGAGACTGGTCAGCCTTGTGTTT	17686
QY	17952	GAGAACTCACAATCCCTTTTATGAGAACACAAATGCTTTCACACTCTCAATGTTATTGGTAA	Db	18767	GGAAAAACAATCTAGTGGCCGAGCTGTAGAGTTTTCAGCGGAGACTGGTCAGCCTTGTGTTT	18011
Db	17687	GAGAACTCACAATCCCTTTTATGAGAACACAAATGCTTTCACACTCTCAATGTTATTGGTAA	QY	19091	TTCCACTCAGAGCTGAAAATGAGCCAGCTTCAGTGAAGCTTGTTCCTTCCCTCCCTCAA	17746
QY	18012	TCCAACTTATCAATATACCTTAAATCACTTAGTACTGAATCTGGCATATAGTATACCTTA	Db	18827	TTCCACTCAGAGCTGAAAATGAGCCAGCTTCAGTGAAGCTTGTTCCTTCCCTCCCTCAA	18071
Db	17747	TCCAACTTATCAATATACCTTAAATCACTTAGTACTGAATCTGGCATATAGTATACCTTA	QY	19151	GGTTACCCACAATCTCAGTTCTCTCAGGAAAGCCAAAAATGAATTTGAGGGTTTAGGA	17806
QY	18072	ATGAGAGATAGAGTCATCGAGTATTTCTGAAGCAATTAGAATCAATAGACTCAATATAC	Db	18887	GGTTACCCACAATCTCAGTTCTCTCAGGAAAGCCAAAAATGAATTTGAGGGTTTAGGA	18131
Db	17807	ATGAGAGATAGAGTCATCGAGTATTTCTGAAGCAATTAGAATCAATAGACTCAATATAC	QY	19211	TTGGTGTCTTTTATCTATTACAGATTGATAATATGTTCTCCACAGAGTGTCTGCTT	17866
QY	18132	ACATGGCAACAAAGTTTGAATCTTAAAGAACCGACTGAGTGAAGGAAAGGAAAGATA	Db	18947	TTGGTGTCTTTTATCTATTACAGATTGATAATATGTTCTCCACAGAGTGTCTGCTT	18191
Db	17867	ACATGGCAACAAAGTTTGAATCTTAAAGAACCGACTGAGTGAAGGAAAGGAAAGATA	QY	19271	GTAAACAATCACTCTCTGACACTTCTGACATATGACAGGAGTGTCTTACCAAGGTAAC	17926
QY	18192	CATAACACGCTACCATATCAATTAATGATAATATATGCTTACCAATTTGTAAAGACACA	Db	19007	GTAAACAATCACTCTCTGACACTTCTGACATATGACAGGAGTGTCTTACCAAGGTAAC	18251
Db	17927	CATAACACGCTACCATATCAATTAATGATAATATATGCTTACCAATTTGTAAAGACACA	QY	19331	ACAGAAATGGCTGCCAATTCCTGAAATCCCTGAACTGAGTGAAGAAATCAGAAATATAT	17986
QY	18252	TACAAATAGATACATGTATATTAATATATCTCGAACGGTTA-CCTATGGGGTGGGCTG	Db	19067	ACAGAAATGGCTGCCAATTCCTGAAATCCCTGAACTGAGTGAAGAAATCAGAAATATAT	18310
Db	17987	TACAAATAGATACATGTATATTAATATATCTCGAACGGTTTACCTATGGGGTGGGCTG	QY	19391	AGGGAAATCAACAGAGCTGGCTACGGATGTGCCAGTGTGACAGTACTTGTCTCATCATAC	18046
QY	18311	GAGTGGGGTAACTCGGTAGCTGTATATGAAACCTTAAACAAATACATGAACAGTAGGA	Db	19067	ACAGAAATGGCTGCCAATTCCTGAAATCCCTGAACTGAGTGAAGAAATCAGAAATATAT	18370
Db	18047	GAGTGGGGTAACTCGGTAGCTGTATATGAAACCTTAAACAAATACATGAACAGTAGGA	QY	19127	AGGGAAATCAACAGAGCTGGCTACGGATGTGCCAGTGGTCAGTACTTGTCTCATCATAC	18106
QY	18371	ATCAGAGAGGTAAACAAATTAATATGTCGCAATGAGAGTGAATTAATCAACTCA	Db	19451	GCAGTGTCTGCTCTAGCAAACTGCTCACTGCTTCAATTTCTGCTGCTTGTCTTTAAATA	18430
Db	18107	ATCAGAGAGGTAAACAAATTAATATGTCGCAATGAGAGTGAATTAATCAACTCA	QY	19187	GCAGTGTCTGCTCTAGCAAACTGCTCACTGCTTCAATTTCTGCTGCTTGTCTTTAAATA	18166
QY	18431	CTGCATCTGAGGTTAAAAATPAGAAAGATGATATGTTATCTTATTAATCTGCTAGTCTT	Db	19511	CTGCTTTTCTCAGCTCAATTTGGCTTTCTTCCCTCTGCGAGTCAGTGTCTTTGGGTCAA	18490
Db	18167	CTGCATCTGAGGTTAAAAATPAGAAAGATGATATGTTATCTTATTAATCTGCTAGTCTT	QY	19247	CTGCTTTTCTCAGCTCAATTTGGCTTTCTTCCCTCTGCGAGTCAGTGTCTTTGGGTCAA	18226
QY	18491	CCAATTGCACTAGCTTTCAATTTGGACTATPCTTCAGATGGCAACCTCTCTGCACTT	Db	19571	CAGCAAAATGATTTCTTAGAATCACCTGGTACTCAAAAGGAGCTACAAGACATTTGGGCATCC	18550
Db	18227	CCAATTGCACTAGCTTTCAATTTGGACTATPCTTCAGATGGCAACCTCTCTGCACTT	QY	19307	CAGCAAAATGATTTCTTAGAATCACCTGGTACTCAAAAGGAGCTACAAGACATTTGGGCATCC	18286
QY	18551	GCTCAGCGAGGAGCTTTTCTCCAGCTTTCTAGTGTGATTTAATATATCAGGNAATA	Db	19631	ACTTCCACTCTTCTGGAAAAACAATTTATGGAAGCCAAAGTTGCCATAGTGCCTCTTGA	18610
Db	18287	GCTCAGCGAGGAGCTTTTCTCCAGCTTTCTAGTGTGATTTAATATATCAGGNAATA	QY	19367	ACTTCCACTCTTCTGGAAAAACAATTTATGGAAGCCAAAGTTGCCATAGTGCCTCTTGA	18346
QY	18611	GTATAAAAAAGGCAAGGCTGCTCCCTGGGTAGCTTTCTGGACTTCAGAGCTAAATTGCA	Db	19691	GCTTGTGTCTCAGCCCAAGGCCCAAGCTTTGTGCTTCAAAACATGAAATTAGAGAGCTTCA	18670
Db	18347	GTATAAAAAAGGCAAGGCTGCTCCCTGGGTAGCTTTCTGGACTTCAGAGCTAAATTGCA	QY	19427	GCTTGTGTCTCAGCCCAAGGCCCAAGCTTTGTGCTTCAAAACATGAAATTAGAGAGCTTCA	18406
QY	18671	AAGTCAGTTTACACATGTGATTTCACTATGAAATTAGGCAAGGTAGAAAACCTGGCAC	Db	19751	GAAACAGATCCACATTTTCAATGGCCTCACCCAACTGGAATAAAGAAACAATTTGCCATATC	18730
Db	18407	AAGTCAGTTTACACATGTGATTTCACTATGAAATTAGGCAAGGTAGAAAACCTGGCAC	QY	19487	GAAACAGATCCACATTTTCAATGGCCTCACCCAACTGGAATAAAGAAACAATTTGCCATATC	18466
QY	18731	AGAAAAATGTGATTTATTTATGTTGTACTATCTCCCTTACAAGCGGAGTGTGAGTGCCTC	Db	19811	TCAATGACCACTTTT-T-CAGGTGGATGGTAGATGCTGGAATGGGTACAGAGCATTTGCC	18790
Db	18467	AGAAAAATGTGATTTATTTATGTTGTACTATCTCCCTTACAAGCGGAGTGTGAGTGCCTC	QY	19547	TCAATGACCACTTTT-T-CAGGTGGATGGTAGATGCTGGAATGGGTACAGAGCATTTGCC	18526
QY	18791	TTTTTGTCCACTGATTTAAGGCAAGTAACTGAAAGTGGCTATGATCACTGCTTTCAAAA	Db	19870	AACCAAACTTTGCAAAAAAGGCTGGAAGCTCTGACTGGGACCCCTAAATATGCAAAAAGTT	18850
Db	18527	TTTTTGTCCACTGATTTAAGGCAAGTAACTGAAAGTGGCTATGATCACTGCTTTCAAAA	QY	19607	AACCAAACTTTGCAAAAAAGGCTGGAAGCTCTGACTGGGACCCCTAAATATGCAAAAAGTT	18586
QY	18851	GCACACTCTGGCCCTCGGCTGAGGCGCTGACATTTCCAGCTGGCTGCGGTGG	Db	19930	GATAGGCTCTTCATGCAAGATAGAACCCGCTGTATGATATAGCTAAAGGTTGGCCTT	18910
Db	18587	GCACACTCTGGCCCTCGGCTGAGGCGCTGACATTTCCAGCTGGCTGCGGTGG	QY	19667	AATAGGCTCTTCATGCAAGATATGAACCCGCTGTATGATATAGCTAAAGGTTGGCCTT	18646
QY	18911	TGACAGTGCATAATTTGGGCGCTTCTGCTGGTGAAGTGTCTCCTTACCTTAGCTCGCTT	Db	19990	TATGTTTCTATTTCTTCCATCAAAACCTGGTAGAATAGATGCTGTTTCCCTTTTAAAAAAT	18970
Db	18647	TGACAGTGCATAATTTGGGCGCTTCTGCTGGTGAAGTGTCTCCTTACCTTAGCTCGCTT	QY	19727	TATGTTTCTATTTCTTCCATCAAAACCTGGTAGAATAGATGCTGTTTCCCTTTTAAAAAAT	18706
QY	18971	GCTGGCACAGCAAGAGAAATCGAAAAATGTTTGGATTTCAAGAGTAAACAAGACT	Db	20050	GTCAACAATTCGATTTATGATGCTGTATAGTAACTCAGATCATGCTCCATGAAAAAT	19030

Db 19787 GTCAACAATTGCAATTTATGATGCTGTGTAATAGTAATCAAGATCATGCTCCATGAAAT 19846
Qy 20110 GCTTCAGAAACCCATATAAGGAGATTTTATAGCCATGTGTGACAAAGAGAGGCCATTC 20169
Db 19847 GCTTCAGAACCCATATAAGGAGATTTTATAGCCATGTGTGACAAAGAGAGGCCATTC 19906
Qy 20170 AGTGTGAAATGCTTCAGAGAAGTATTCATTAATGTTTCTCAGATCTTTTATTTTAT 20229
Db 19907 AGTGTGAAATGCTTCAGAGAAGTATTCATTAATGTTTCTCAGATCTTTTATTTTAT 19966
Qy 20230 TTTTGTGAAACAGAGCTCTACATTTCTCACCAGGCTGGAGTACAGTGCTGTGCTCG 20289
Db 19967 TTTTGTGAAACAGAGCTCTACATTTCTCACCAGGCTGGAGTACAGTGCTGTGCTCG 20026
Qy 20290 GCTCACTGCAACCTCTGCTCCAGGTTCCAGGATTCCTGTGACGTTCCCGAATAGC 20349
Db 20027 GCTCACTGCAACCTCTGCTCCAGGTTCCAGGATTCCTGTGACGTTCCCGAATAGC 20086
Qy 20350 TGGGATACAGGCGCATGACACCACTGCTAATTTTGTATTTTATAGTAGACAGAGT 20409
Db 20087 TGGGATACAGGCGCATGACACCACTGCTAATTTTGTATTTTATAGTAGACAGAGT 20146
Qy 20410 TTCGCCATGTTGACCGGCTTGCTTGAACCTCTGACTTCAGTGATCCACCCACTCAG 20469
Db 20147 TTCGCCATGTTGACCGGCTTGCTTGAACCTCTGACTTCAGTGATCCACCCACTCAG 20206
Qy 20470 CTTCCCAAGCACTGGATACAGGATGACGACCGTCCGACGCTGTTTCTCAGATC 20529
Db 20207 CTTCCCAAGCACTGGATACAGGATGACGACCGTCCGACGCTGTTTCTCAGATC 20266
Qy 20530 CTGTA-TTTGTTCTGAGGCTTCATTTCTATCTTATTTTGAAGTAGTACAC 20588
Db 20267 CTGTA-TTTGTTCTGAGGCTTCATTTCTATCTTATTTTGAAGTAGTACAC 20326
Qy 20589 CTAAGTAAGGTTTTTAACAATCAAAATATCTTTGGAAATTCCTGTTCTTTCTATTC 20648
Db 20327 CTAAGTAAGGTTTTTAACAATCAAAATATCTTTGGAAATTCCTGTTCTTTCTATTC 20386
Qy 20649 CTACAAAATATGTCAGTATAGCTGATGTTTCTTCAAAATATTCATTTCTCTA 20708
Db 20387 CTACAAAATATGTCAGTATAGCTGATGTTTCTTCAAAATATTCATTTCTCTA 20446
Qy 20709 TCTCAGAAATTTATCTCATGCTTAATTTGTAATGATCTTCACATTCCTGTCATCCAGT 20768
Db 20447 TCTCAGAAATTTATCTCATGCTTAATTTGTAATGATCTTCACATTCCTGTCATCCAGT 20506
Qy 20769 TTTGTTGCTCTATTTTCACTCTAAGCTAAGTGGCTATTAGATTAAGAGCTTGTAAACAG 20828
Db 20507 TTTGTTGCTCTATTTTCACTCTAAGCTAAGTGGCTATTAGATTAAGAGCTTGTAAACAG 20566
Qy 20829 ATTCTTTCTCCAATATGCTTTATCTTTTGACTGCATGCCAGTGACAAACTGTTAACTGT 20888
Db 20567 ATTCTTTCTCCAATATGCTTTATCTTTTGACTGCATGCCAGTGACAAACTGTTAACTGT 20626
Qy 20889 TTGATTTCTTATAACATTCACAGAACATGCTGACTCTCTCTCTGTAAGCAATGCC 20948
Db 20627 TTGATTTCTTATAACATTCACAGAACATGCTGACTCTCTCTCTGTAAGCAATGCC 20686
Qy 20949 AAGCACAGCATTTGTAGATAGTATGTACGCAACAGGAGCATGGTGATAGCAAAACTA 21008
Db 20687 AAGCACAGCATTTGTAGATAGTATGTACGCAACAGGAGCATGGTGATAGCAAAACTA 20746
Qy 21009 GAAGGAAGAGGACCTTCTTCTAGCAATGGGTGATATGGTCCCTGGACTTAGACTCCAAAG 21068
Db 20747 GAAGGAAGAGGACCTTCTTCTAGCAATGGGTGATATGGTCCCTGGACTTAGACTCCAAAG 20806
Qy 21069 GGTGCTGAGTGAAACACACATCGTCCATACCCAGGAAGCACACAGTGGGATGGAAGAG 21128
Db 20807 GGTGCTGAGTGAAACACACATCGTCCATACCCAGGAAGCACACAGTGGGATGGAAGAG 20866
Qy 21129 CTGTGCTTAATGAACTTCTCATCCAGTGGAGGTGGAGGAGGCTGCAAGTCA 21188
Db 20867 CTGTGCTTAATGAACTTCTCATCCAGTGGAGGTGGAGGAGGCTGCAAGTCA 20926

Qy 21189 GAGCTGCTTACCCAGACAGAGGACAGGAGGCGCTTTCTGGAGGAAACAGCCTCTGAAAC 21248
Db 20927 GAGCTGCTTACCCAGACAGAGGACAGGAGGCGCTTTCTGGAGGAAACAGCCTCTGAAAC 20986
Qy 21249 TGGCAGCTGATAGAGAGCTCTACCTCAACTCTTCTGGTTCCTCCAGGGTGTCTTTCCAC 21308
Db 20987 TGGCAGCTGATAGAGAGCTCTACCTCAACTCTTCTGGTTCCTCCAGGGTGTCTTTCCAC 21046
Qy 21309 GTCCATTTATGGCACTGAAAGTTTGAATACCTTCAGGGGCCGAAAGCCTGCCAGTCT 21368
Db 21047 GTCCATTTATGGCACTGAAAGTTTGAATACCTTCAGGGGCCGAAAGCCTGCCAGTCT 21106
Qy 21369 CTTCCTGCGAGAGCAATCACACCAACCTGCAAGGCTAGGAAAGGCTGTCTATCATCTC 21428
Db 21107 CTTCCTGCGAGAGCAATCACACCAACCTGCAAGGCTAGGAAAGGCTGTCTATCATCTC 21166
Qy 21429 CTACTCAGAAACTGGTTTCACTGGAAGACTCAGGGGCCACTGAAATACATCTCGGAGCTT 21488
Db 21167 CTACTCAGAAACTGGTTTCACTGGAAGACTCAGGGGCCACTGAAATACATCTCGGAGCTT 21226
Qy 21489 TCACAAGAGGGCTTCTGACTCAAGGATGTTTCCATCTTTGCCAGGTTCGCTTTCTCTCT 21548
Db 21227 TCACAAGAGGGCTTCTGACTCAAGGATGTTTCCATCTTTGCCAGGTTCGCTTTCTCTCT 21286
Qy 21549 TCTCTTAGAGTTTGGAGGACGCAAAATGTCTGAGAACTCAACCTTTCTGCAAGGTGAGA 21608
Db 21287 TCTCTTAGAGTTTGGAGGACGCAAAATGTCTGAGAACTCAACCTTTCTGCAAGGTGAGA 21346
Qy 21609 CACAAGGGCTTTCCAGAGCAAGAGAGAGCAAAATGGAAGTCTCTTCTCTCCAGTA 21668
Db 21347 CACAAGGGCTTTCCAGAGCAAGAGAGCAAAATGGAAGTCTCTTCTCTCCAGTA 21406
Qy 21669 GAGGATCGACTGTCTGGCAGGACCCCAACAGGAAAGACAAATGATGATGCTGCTGCTGT 21728
Db 21407 GAGGATCGACTGTCTGGCAGGACCCCAACAGGAAAGACAAATGATGATGCTGCTGT 21466
Qy 21729 TCCCTCCCTCCCTCCCTTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 21788
Db 21467 TCCCTCCCTCCCTCCCTTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 21526
Qy 21789 CCCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 21848
Db 21527 CCCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 21586
Qy 21849 CTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 21908
Db 21587 CTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 21646
Qy 21909 CTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 21968
Db 21647 CTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 21706
Qy 21969 TCTTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 22028
Db 21707 TCTTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 21766
Qy 22029 CATCTCATTAATGCTGAATGCTGCCCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 22088
Db 21767 CATCTCATTAATGCTGAATGCTGCCCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 21826
Qy 22089 GGAAGCCACTTTCCTTTTACTGAAATTAATAATAGTAAAGAGCTAAAAATTAATGTTA 22148
Db 21827 GGAAGCCACTTTCCTTTTACTGAAATTAATAATAGTAAAGAGCTAAAAATTAATGTTA 21886
Qy 22149 AAAATGACGATTAATAATAGTAAATTAATAATAGTAAAGAGCTAAAAATTAATGTTA 22208
Db 21887 AAAATGACGATTAATAATAGTAAATTAATAATAGTAAAGAGCTAAAAATTAATGTTA 21946
Qy 22209 AAAAGCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 22268
Db 21947 AAAAGCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 22006

QY	22269	ATTAGTTGGAGAACCAACATCAGAGAAAAATAGATACCTGTGTATAGTCACTGTGTATCTTA	22328	Db	23087	TGTAGGCCCAACTATGTTTTTAAAGAGTTTTTTTTTAAAGGATATCTGCTGAACCAATC	23146
Db	22007	ATTAGTTGGAGAACCAACATCAGAGAAAAATAGATACCTGTGTATAGTCACTGTGTATCTTA	22066	QY	23408	ATGCCACCAACCAAGAGTGAAGACTATAAAACATACCCAGCTTTTTCAAAGCATTTAAAA	23467
QY	22329	TGGNATTAACATTTGTAGAGAAAATCTGGACATGATCTCTTTCTGAGTAAAGAGAGCTGGGT	22388	Db	23147	ATGCCACCAACCAAGAGTGAAGACTATAAAACATACCCAGCTTTTTCAAAGCATTTAAAA	23206
Db	22067	TGGNATTAACATTTGTAGAGAAAATCTGGACATGATCTCTTTCTGAGTAAAGAGAGCTGGGT	22126	QY	23468	ATTATTTCAAATAATTTTTTCTCAGAAAAATTTTGCATTGATTCCTCGAAGAACATTAA	23527
QY	22389	ACAATTAAGGGGAGATTGAAAGGAATCCAAAAGCATAGACAGATGCTGTGCTCACTGGAA	22448	Db	23207	ATTATTTCAAATAATTTTTTCTCAGAAAAATTTTGCATTGATTCCTCGAAGAACATTAA	23266
Db	22127	ACAATTAAGGGGAGATTGAAAGGAATCCAAAAGCATAGACAGATGCTGTGCTCACTGGAA	22186	QY	23528	TATGGGACCTGACCTTATAAATATGAATCAATCTCCCACTCAAGTAGGAGTCTCTC	23587
QY	22449	TGGTTGCCGATCTCTCCAAACTATGAAGTGTGTGAGGCTCAACTTTTAATATAATTAAGA	22508	Db	23267	TATGGGACCTGACCTTATAAATATGAATCAATCTCCCACTCAAGTAGGAGTCTCTC	23326
Db	22187	TGGTTGCCGATCTCTCCAAACTATGAAGTGTGTGAGGCTCAACTTTTAATATAATTAAGA	22246	QY	23588	AGATTTAAAAAATAAGCATCTAGTCTCTTGTCTCTGCTAAAGATTAAACCTTACACCTG	23647
QY	22509	TACAAAGACAGATGAGAGAAAAGAGAGAGGGAGCTCACTGGAGAACACTCAAGATTCC	22568	Db	23327	AGATTTAAAAAATAAGCATCTAGTCTCTTGTCTCTGCTAAAGATTAAACCTTACACCTG	23386
Db	22247	TACAAAGACAGATGAGAGAAAAGAGAGAGGGAGCTCACTGGAGAACACTCAAGATTCC	22306	QY	23648	AAACACAGGAGACTGGCGGTTGTTTGCATAGGGGTTTACAAATAAAGTTGAGCTACCTCT	23707
QY	22569	TTACTACTCAATCTCTAAATAATCAATTTGTTAGATGGAAAAAGAAAAAGCTTCTCTG	22628	Db	23387	AAACACAGGAGACTGGCGGTTGTTTGCATAGGGGTTTACAAATAAAGTTGAGCTACCTCT	23446
Db	22307	TTACTACTCAATCTCTAAATAATCAATTTGTTAGATGGAAAAAGAAAAAGCTTCTCTG	22366	QY	23708	GACATCTATTAAACCAAAAATTAGTAACTATGATGATGAGAGACTTTTATGATTGAAC	23767
QY	22629	TTAAAAAGGAGCTTGTCTATAGGAGGTTTAAAAATATACTCTGACCCATCTCCAACAT	22688	Db	23447	GACATCTATTAAACCAAAAATTAGTAACTATGATGATGAGAGACTTTTATGATTGAAC	23506
Db	22367	TTAAAAAGGAGCTTGTCTATAGGAGGTTTAAAAATATACTCTGACCCATCTCCAACAT	22426	QY	23768	TTGTTTATTGAGTCAAGAGATATAGTTTACAAATAAATAATTTGGGCGCATATCAAAATGACC	23827
QY	22689	TCTAAATCTCTCCAGAAAAGTAGTGCATCCCAAGAAATATTTCAATCAAAATGCTGGAA	22748	Db	23507	TTGTTTATTGAGTCAAGAGATATAGTTTACAAATAAATAATTTGGGCGCATATCAAAATGACC	23566
Db	22427	TCTAAATCTCTCCAGAAAAGTAGTGCATCCCAAGAAATATTTCAATCAAAATGCTGGAA	22486	QY	23828	TTGCTTAGCTTAGCATTTGCTGATGTTTAACTATTTTCTCATTTGGGCTGATTTTAGTTG	23887
QY	22749	AGAAAAATCAAAATATTAATAATGATTTAGGAAGCAGACAGTAAATTAATCAGAACTGGAG	22808	Db	23567	TTGCTTAGCTTAGCATTTGCTGATGTTTAACTATTTTCTCATTTGGGCTGATTTTAGTTG	23626
Db	22487	AGAAAAATCAAAATATTAATAATGATTTAGGAAGCAGACAGTAAATTAATCAGAACTGGAG	22546	QY	23888	CTTAGGAAAAATACAAACACACACACTTTAAAAATTTATTAATAATCCGCTCTAAACCTC	23947
QY	22809	CAGGAATAGACAGCAGATCAATGAGACAGACATCAAGTCCCGAATGTGGACTTGCAA	22868	Db	23627	CTTAGGAAAAATACAAACACACACACTTTAAAAATTTATTAATAATCCGCTCTAAACCTC	23686
Db	22547	CAGGAATAGACAGCAGATCAATGAGACAGACATCAAGTCCCGAATGTGGACTTGCAA	22606	QY	23948	AGAGTCCAGAACCCATCTTAACACTGGTTCATGCAATATATGTTTAAATTTTGTGCTTT	24007
QY	22869	TGCATTAAGTAATATGATATGCAATAAAGTGSCACAGTGAACCAATGGGAAAAAATTA	22928	Db	23687	AGAGTCCAGAACCCATCTTAACACTGGTTCATGCAATATATGTTTAAATTTTGTGCTTT	23746
Db	22607	TGCATTAAGTAATATGATATGCAATAAAGTGSCACAGTGAACCAATGGGAAAAAATTA	22666	QY	24008	AAAACTACAATAAAGAAATGTTTAAATAGTTTCCACAACTCAATGGTCAAGTTAGCGAGG	24067
QY	22929	ATCTTATAATATGATATGCAATAATGCTCTAGTAAATTTGGGGAAGAAATAAGCTTAT	22988	Db	23747	AAAACTACAATAAAGAAATGTTTAAATAGTTTCCACAACTCAATGGTCAAGTTAGCGAGG	23806
Db	22667	ATCTTATAATATGATATGCAATAATGCTCTAGTAAATTTGGGGAAGAAATAAGCTTAT	22726	QY	24068	AAGATTAGCATAGTTAAAGACTTAAAAATGGCTTTTACAACTATATCAAAAGGACAAAATA	24127
QY	22989	TCCTTATCTCAATTTCTTTTCTTTTGGAGACAGAGTCTCACTCTGTGTAGCCAGGCTG	23048	Db	23807	AAGATTAGCATAGTTAAAGACTTAAAAATGGCTTTTACAACTATATCAAAAGGACAAAATA	23866
Db	22727	TCCTTATCTCAATTTCTTTTCTTTTGGAGACAGAGTCTCACTCTGTGTAGCCAGGCTG	22786	QY	24128	AGGGAAACAGAGTCTAGAAATGAGGAAAATCTGGGACACAGGCAAAAAAATAATGAGAAC	24187
QY	23049	GAGTGACGAGATCGATCTCTGCCACTGCAACCTTGTCTCTCCGGGCTCAGCGATTTCT	23108	Db	23857	AGGGAAACAGAGTCTAGAAATGAGGAAAATCTGGGACACAGGCAAAAAAATAATGAGAAC	23926
Db	22787	GAGTGACGAGATCGATCTCTGCCACTGCAACCTTGTCTCTCCGGGCTCAGCGATTTCT	22846	QY	24188	TGGGACATGAATAACGCAAGSGATAAGACTAAATACACAAACACCCCAAAATAATAGCCA	24247
QY	23109	CCCACTCAGCCTCCCGAGCAGCTGAACCTACAGGGGCTGTGCCACCACTCCCGGCAATTTT	23168	Db	23927	TGGGACATGAATAACGCAAGSGATAAGACTAAATACACAAACACCCCAAAATAATAGCCA	23986
Db	22847	CCCACTCAGCCTCCCGAGCAGCTGAACCTACAGGGGCTGTGCCACCACTCCCGGCAATTTT	22906	QY	24248	GCATTTGCTGAGCTCTTACTGTGAGCTGTGTTCTTAAGCACTTTTACATATATTAATCAATTT	24307
QY	23169	TTTTTCCATTTTGTAGTAAATAATGGGTTTCAACATGTCCTGGGCTGTGCTGTGAACCTC	23228	Db	23987	GCATTTGCTGAGCTCTTACTGTGAGCTGTGTTCTTAAGCACTTTTACATATATTAATCAATTT	24046
Db	22907	TTTTTCCATTTTGTAGTAAATAATGGGTTTCAACATGTCCTGGGCTGTGCTGTGAACCTC	22966	QY	24308	CATCTCAAGGAACCACTGAGGAGGAGCTGTGTTATCATCTCCATTTTACAGATAAGGAA	24367
QY	23229	TGGGCTCAGGCAATCCACCGCTTGGCTCCCAAGTGTCTAGCATTTACAGGCAATGAGCC	23288	Db	24047	CATCTCAAGGAACCACTGAGGAGGAGCTGTGTTATCATCTCCATTTTACAGATAAGGAA	24106
Db	22967	TGGGCTCAGGCAATCCACCGCTTGGCTCCCAAGTGTCTAGCATTTACAGGCAATGAGCC	23026	QY	24368	TAGACCCAGAGAGGCTGAGCAACTTTGGGCTATTCCACAGCTACTATGTTGGAGATGAGAT	24427
QY	23289	ACCGGCTTGGAGCTCAATTTCTTAGACTAAATAATTTGGAGATGGCTAAAGATTTCTTA	23348	Db	24107	TAGACCCAGAGAGGCTGAGCAACTTTGGGCTATTCCACAGCTACTATGTTGGAGATGAGAT	24166
Db	23027	ACCGGCTTGGAGCTCAATTTCTTAGACTAAATAATTTGGAGATGGCTAAAGATTTCTTA	23086	QY	24428	TTAAATCTAATCTATTTGCTCCAGAGCCCATGCAACCAATGGCTGCATTAAGTGAATGCAT	24487
QY	23349	TGTAGGCCAACTATGTTTTTAAAAAG-TTTTTTTTTTAAAGGATACTGCTGGAAACAATC	23407				

QY	26644	ACCTCTTTGACHTCTCTATGCCCTGTGTCATTCACCTCATGGGTCTTTATTACATTAATTGCAT	26703
Db	26384	ACCTCTTTGACTTCTCTATGCCCTGTCAVTCACCTCATGGGTCTTTATTACATTAATTGCAT	26443
QY	26704	CTGTGTCAAATAACTCTGGTCTTTCTGTGTTAAAGTTCAGTCCAGTCTCCCAATTTCAAATGTCGCCA	26763
Db	26444	CTGTGTCAAATAACTCTGGTCTTTCTCTTAAGTTCAGTCTCCCAATTTCAAATGTCGCCA	26503
QY	26764	GACATTTCCAAATGAGTATCTCTCCAAATGATTAATTAACCTGCTAAATATCTAAACACATAAT	26823
Db	26504	GACATTTCCAAATGAGTATCTCTCCAAATGATTAATTAACCTGCTAAATATCTAAACACATAAT	26563
QY	26824	CTTTCCCATCAAAATCGTTTCCTCTTAAGCTTTTGGTATTTCTATAGACTCTCGCACT	26883
Db	26564	CTTTCCCATCAAAATCGTTTCCTCTTAAGCTTTTCTTATTTCTTAATAGTACTCTCGCACT	26623
QY	26884	TCTCCAGAGCCAGAGACTTTAAACCTTGAATTTCTCACATAACCTCTCTTTTGTCTCC	26943
Db	26624	TCTCCAGAGCCAGAGACTTTAAACCTTGAATTTCTCACATAACCTCTCTTTTGTCTCC	26583
QY	26944	CATTAATCAATTAGTAGCAAGTGTTATCAATGATTAATCTGACATAATCTTTTCTATTTC	27003
Db	26684	CATTAATCAATTAGTAGCAAGTGTTATCAATGATTAATCTGACATAATCTTTTCTATTTC	26743
QY	27004	CTCCCTGCTATGATCAATTCATCTAGCAAGAAGAGTTGGCCCTTTGTATCTGCGTTCTG	27063
Db	26744	CTCCCTGCTATGATCAATTCATCTAGCAAGAAGAGTTGGCCCTTTGTATCTGCGTTCTG	26803
QY	27064	CATCCCTGGATCAACCAACTGATAGTGGAAAAATTTTCAAGAAAAAAGCGTCTATCTG	27123
Db	26804	CATCCCTGGATCAACCAACTGATAGTGGAAAAATTTTCAAGAAAAAAGCGTCTATCTG	26863
QY	27124	AGTATGAAAAAATTTTATTTCTTGCTCATTTATTCCTTAAACATACAGTATACCACTACA	27183
Db	26864	AGTATGAAAAAATTTTATTTCTTGCTCATTTATTCCTTAAACATACAGTATACCACTACA	26923
QY	27184	GCATTTACCTGTAGCTATAGATCTTATAATCTAGAAATGATTTCAAGTACACCATTAAT	27243
Db	26924	GCATTTACCTGTAGCTATAGATCTTATAATCTAGAAATGATTTCAAGTACACCATTAAT	26983
QY	27244	ATATAAGGACTTGAGCATCTGTGAAGTTGGTATTTGTGGGGGATACGGGACCAATTC	27303
Db	26984	ATATAAGGACTTGAGCATCTGTGAAGTTGGTATTTGTGGGGGATACGGGACCAATTC	27043
QY	27304	CCCCATGGATACAGAGGGCAACTATATTTACTTCAGTGCTTACTAAATACAGATTGGCCA	27363
Db	27044	CCCCATGGATACAGAGGGCAACTATATTTACTTCAGTGCTTACTAAATACAGATTGGCCA	27103
QY	27364	ATGTGTTTTTCTTTTCTGTTTTCTGTCTTTTAGTTTGGCCCTTGCCCAATTAATCAATA	27423
Db	27104	ATGTGTTTTTCTTTTCTGTTTTCTGTCTTTTAGTTTGGCCCTTGCCCAATTAATCAATA	27163
QY	27424	GTGCTGCCAATGCCAGGTGACCTTCCAGATAATCTATTCTAAATTTTCGTCATCTCCAGC	27483
Db	27164	GTGCTGCCAATGCCAGGTGACCTTCCAGATAATCTATTCTAAATTTTCGTCATCTCCAGC	27223
QY	27484	TTAAAAATATTTAATGGGCCAGCGCAGTGGTCACTTTGTAATCCAGCATTTTGGGA	27543
Db	27224	TTAAAAATATTTAATGGGCCAGCGCAGTGGTCACTTTGTAATCCAGCATTTTGGGA	27283
QY	27544	GGCCAGGGGGGTGTATCATCTTGAGGTCCAGAGTTCCAGACCAGCTGGGCCACATGGC	27603
Db	27284	GGCCAGGGGGGTGTATCATCTTGAGGTCCAGAGTTCCAGACCAGCTGGGCCACATGGC	27343
QY	27604	GAATCCCTGTCTCTACAAAAAGTATPAAAGTTAAACCAGGTGCTGGAGCATTTGCCTGTG	27663
Db	27344	GAATCCCTGTCTCTACAAAAAGTATPAAAGTTAAACCAGGTGCTGGAGCATTTGCCTGTG	27403
QY	27664	GTCCAGCTACTCAGAGGCTGAGGCAGAAAAATCATTTTAATCTGGGAGGTGGAGTTTG	27723
Db	27404	GTCCAGCTACTCAGAGGCTGAGGCAGAAAAATCGCTTAACTGGGAGGTGGAGTTTG	27463
QY	27724	CAGTGAAGCCAAAGATCTCTCACTGCTCACTCCAGCTGGGTGACACAGCAAGACTCTATCTC	27783

Db	27464	CAGTGGCCAAAGATCTCTCCACTGCACTCCAGCTGGGTGACACAGCAAGACTCTATCTC	27523
Qy	27784	AAAAACAACATPAACAACAACAAGAAAAACATTTAATGCTGCACCTTGCCTGTGAAAAA	27843
Db	27524	AAAAACAACATPAACAACAACAAGAAAAACATTTAATGCTGCACCTTGCCTGTGAAAAA	27583
Qy	27844	TGCATTTCTTTGGCCAGATGTGGTGTCAAACTGTAAATCCCAACACTTTGGGAAGCTAA	27903
Db	27584	TGCATTTCTTTGGCCAGATGTGGTGTCAAACTGTAAATCCCAACACTTTGGGAAGCTAA	27643
Qy	27904	GGCCAGAGTTTGAGACGAGCTGGGATATATAGGAAGACACAATCTCTACAAAAAAAAT	27963
Db	27644	GGCCAGAGTTTGAGACGAGCTGGGATATATAGGAAGACACAATCTCTACAAAAAAAAT	27703
Qy	27964	CCACAAAATTAGTCAGCTTATTTGTCATGCCCTGTAGTCCCAAGTACTCAGAGGCTGAG	28023
Db	27704	CCACAAAATTAGTCAGCTTATTTGTCATGCCCTGTAGTCCCAAGTACTCAGAGGCTGAG	27763
Qy	28024	GCAGGATTCCTCAAGCCCAAGGAGTTCAAGGCTTCGCTGAGCTATGATGGCACTCACTGCAC	28083
Db	27764	GCAGGATTCCTCAAGCCCAAGGAGTTCAAGGCTTCGCTGAGCTATGATGGCACTCACTGCAC	27823
Qy	28084	TCCATCTTTGGGTGACAGACGAGTCTCTATCTCTGGAGAAAAAAAAGAGAGGCATTT	28143
Db	27824	TCCATCTTTGGGTGACAGACGAGTCTCTATCTCTGGAG - AAAAAAAGAGAGAGGCATTT	27882
Qy	28144	TCTTAGGAGAGTTCTTCTCTGTAGAGTCCCTAAGGTTCCATGGAACTCTTTAAAGCATC	28203
Db	27883	TCTTAGGAGAGTTCTTCTCTGTAGAGTCCCTAAGGTTCCATGGAACTCTTTAAAGCATC	27942
Qy	28204	AGAGTATGAGTGCATATGGGAGGAAGCATTTAGCCAGAGCATTTGTGCTCCCATTTGCAT	28263
Db	27943	AGAGTATGAGTGCATATGGGAGGAAGCATTTAGCCAGAGCATTTGTGCTCCCATTTGCAT	28002
Qy	28264	ATTAAATTTTAAAAAACAAGCTATAAAAAAGTTGAAACTACTAGTTAGCATCAGC	28323
Db	28003	ATTAAATTTTAAAAAACAAGCTATAAAAAAGTTGAAACTACTAGTTAGCATCAGC	28062
Qy	28324	CTGACATTTAATGGCTCTGTAATCAAACTTAAATGTACTTTTAGCCAGTTATGCTACT	28383
Db	28063	CTGACATTTAATGGCTCTGTAATCAAACTTAAATGTACTTTTAGCCAGTTATGCTACT	28122
Qy	28384	AGCCAACTACAGACAACACATTTTAAACCAATTAGACTAATAGTGTCTATCAGTGGAA	28443
Db	28123	AGCCAACTACAGACAACACATTTTAAACCAATTAGACTAATAGTGTCTATCAGTGGAA	28182
Qy	28444	ATCAAGTTTGCCATTTCCATGCCCTTTGCTCACACCAATACCTTTCTGGAATGTCTGT	28503
Db	28183	ATCAAGTTTGCCATTTCCATGCCCTTTGCTCACACCAATACCTTTCTGGAATGTCTGT	28242
Qy	28504	TACTCATCTCTCTGTGTGAACTCTATACCCAACTTTAAAAACCTAGCTCAAGTTCAAC	28563
Db	28243	TACTCATCTCTCTGTGTGAACTCTATACCCAACTTTAAAAACCTAGCTCAAGTTCAAC	28302
Qy	28564	ACTTCCATTTCCATTTCAAAAAAGCTTTCCCTCTCTTTAAAGTTTAAAGACTCATTTTCA	28623
Db	28303	ACTTCCATTTCCATTTCAAAAAAGCTTTCCCTCTCTTTAAAGTTTAAAGACTCATTTTCA	28362
Qy	28624	TGAATCTTTTGGCACTTATTCGACACATGCTGTGCTTTGTGTTATTTGTGTTCA - GCCTC	28682
Db	28363	TGAATCTTTTGGCACTTATTCGACACATGCTGTGCTTTGTGTTATTTGTGTTCA	28422
Qy	28683	ATATGCCCCAAGGTGTTTATGACTCTTTAAGCGCAAAATGATGCTCTAAACACCTTTC	28742
Db	28423	ATATGCCCCAAGGTGTTTATGACTCTTTAAGCGCAAAATGATGCTCTAAACACCTTTC	28482
Qy	28743	TATCTTTTCAAGTGTCTTAGTCTGTTTGTGTTGTTGTTTAAAGGAATACCTGAGGCTGGGA	28802
Db	28483	TATCTTTTCAAGTGTCTTAGTCTGTTTGTGTTGTTTAAAGGAATACCTGAGGCTGGGA	28542
Qy	28803	ATTATTTTAAAAAAGAGGTTTATTTGGCTCACAGTCTGCGAGCTATATAGAGCATAGT	28862

Db 28543 ATTATTTAAAAAGAGGTTTATTGGCTCAGTTTCTGCAGCTATATAGAGCATAGT 28602
Qy 28863 GTGAGCATCTGCTTTCAGGTGAGGGCTTCAGGAAGTTTCCACCCTAGGTAGAGGCAAGG 28922
Db 28603 GTGAGCATCTGCTTTCAGGTGAGGGCTTCAGGAAGTTTCCACCCTAGGTAGAGGCAAGG 28662
Qy 28923 GGAGCGGCAATCATATCAAGAGAGGAGGAAAAAGAAAGAAAGAAAGAGGGGTGCCA 28982
Db 28663 GGAGCGGCAATCATATCAAGAGAGGAGGAAAAAGAAAGAAAGAAAGAGGGGTGCCA 28722
Qy 28983 TTCTCTTTCAACAATCAGTTCTTTGTCGGAACTAATGGGCAAGAGAGCTGGGCAACGGTGGC 29042
Db 28723 TTCTCTTTCAACAATCAGTTCTTTGTCGGAACTAATGGGCAAGAGAGCTGGGCAACGGTGGC 28782
Qy 29043 TCATGCTGTAAATCCAGGCCCTTTGGGAGACCAAGGTGGTGGATCACCTGAAGTCAGAA 29102
Db 28783 TCATGCTGTAAATCCAGGCCCTTTGGGAGACCAAGGTGGTGGATCACCTGAAGTCAGAA 28842
Qy 29103 CCTGAGACCGCTGGCCAAATGTGTGGAACCTCCGCTCTACTAAAAATACAAAAAT-- 29160
Db 28843 GCCTGAGACCGCTGGCCAAATGTGTGGAACCTCCGCTCTACTAAAAATACAAAAATTA 28902
Qy 29161 ----TAGCTGGGCTGGTGGCGGTGTACCTGTAGTCCAGATACTCAGGAGGCTGAGGTAG 29216
Db 28903 GATCTAGCTGGGCTGGTGGCGGTGTACCTGTAGTCCAGATACTCAGGAGGCTGAGGTAG 28962
Qy 29217 GATTAATCACTTGAACCCGGAGACAGAGTTGAGTGGCTGAGCTGAGCTGAGCTCCAGC 29276
Db 28963 GATAATCACTTGAACCCGGAGACAGAGTTGAGTGGCTGAGCTGAGCTGAGCTCCAGC 29022
Qy 29277 CGGGCAACAGAGTGAGCGGTCTCAAAAAATTTTAAAAAATTTAAAAAATATAGAGCAA 29336
Db 29023 CGGGCAACAGAGTGAGCGGTCTCAAAAAATTTTAAAAAATTTAAAAAATATAGAGCAA 29082
Qy 29337 GAAAGCAACCAAGTTATTCAGGAGGGATCCACCCCAATGACTCAATATCTCCACCAGG 29396
Db 29083 GAAAGCAACCAAGTTATTCAGGAGGGATCCACCCCAATGACTCAATATCTCCACCAGG 29142
Qy 29397 CCTCACTTCCAACTGGGATCAATTTCCGTATGAGTTTGAGAGAGCAAAATATCCAA 29456
Db 29143 CCTCACTTCCAACTGGGATCAATTTCCGTATGAGTTTGAGAGAGCAAAATATCCAA 29202
Qy 29457 ACTATATCATATAGTAATGAACATAGTACCTTATCTATAGAAAGCAATGGCTAGACAAT 29516
Db 29203 ACTATATCATATAGTAATGAACATAGTACCTTATCTATAGAAAGCAATGGCTAGACAAT 29262
Qy 29517 GTTGAATGGCTAACCAATCTGCTTTCCCTATGCTCGCTCTAGAGGGGTGAGTATGAG 29576
Db 29263 GTTGAATGGCTAACCAATCTGCTTTCCCTATGCTCGCTCTAGAGGGGTGAGTATGAG 29322
Qy 29577 TTTCTGTCAAAAGAGAGAAAAAATGATATAGTACGTTTTGTGTGTGTGTGTTCATGT 29636
Db 29323 TTTCTGTCAAAAGAGAGAAAAAATGATATAGTACGTTTTGTGTGTGTGTGTTCATGT 29382
Qy 29637 AAAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 29696
Db 29383 AAAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 29442
Qy 29697 ATACATAGAAAAAGCAAAATTTATCTGTTTATCAGTAATACCCAAAGGGGTAGAAATGGT 29756
Db 29443 ATACATAGAAAAAGCAAAATTTATCTGTTTATCAGTAATACCCAAAGGGGTAGAAATGGT 29502
Qy 29757 AAGTAATAATCTTCTTCACTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29816
Db 29503 AAGTAATAATCTTCTTCACTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29562
Qy 29817 ATTACATCGAGACATTAATCACTTAAGGCTTCCAAATTTTGGAGATAGAAAGGGCT 29876
Db 29563 ATTACATCGAGACATTAATCACTTAAGGCTTCCAAATTTTGGAGATAGAAAGGGCT 29622
Qy 29877 GCTATGCTTTATAGATGGAAGAACTTTGGGTCAATTAATCTCAAAACAGGACATAACAA 29936
Db 29628 GCTATGCTTTATAGATGGAAGAACTTTGGGTCAATTAATTAATCTCAAAACAGGACATAACAA 29682

Qy 29937 AGAATGGAGCATAAACTGCCAGTCTGACTGTAGATTTGGATTTCCAGTTGGTGTCTT 29996
Db 29683 AGAATGGAGCATAAACTGCCAGTCTGACTGTAGATTTGGATTTCCAGTTGGTGTCTT 29742
Qy 29997 GTCAACCTTTGTTTACTCTTCTTAAAGTTATGATCTTTTCTGTGCATAGAGAAATTCATAG 30056
Db 29743 GTCAACCTTTGTTTACTCTTCTTAAAGTTATGATCTTTTCTGTGCATAGAGAAATTCATAG 29802
Qy 30057 TGATTTCCCATACCCCTTGGGATTCATAGCTCTTAAAGTCCCTTAAAGTCCCTTATGCATCTAA 30116
Db 29803 TGATTTCCCATACCCCTTGGGATTCATAGCTCTTAAAGTCCCTTATGCATCTAA 29862
Qy 30117 TAACATCAACAGTAAGTGTCTTTTCGAGCACTTACTGAGTGTATATCATTTGTGTCTCAGC 30176
Db 29863 TAACATCAACAGTAAGTGTCTTTTCGAGCACTTACTGAGTGTATATCATTTGTGTCTCAGC 29922
Qy 30177 CAGCACCCACAGATCTCAACAGAACTAGCTGAAGCCCTGTAGAAATAGTAAGTATAGTAC 30236
Db 29923 CAGCACCCACAGATCTCAACAGAACTAGCTGAAGCCCTGTAGAAATAGTAAGTATAGTAC 29982
Qy 30237 TGCCATGCCAATCTGGAGTACTCAAGCGATGCAAAATGATTCCTTTAATTGTACTTTTGA 30296
Db 29983 TGCCATGCCAATCTGGAGTACTCAAGCGATGCAAAATGATTCCTTTAATTGTACTTTTGA 30042
Qy 30297 GGCTTGTCACTTTTGTCTCATGGAGAGTGGCTACTGCATCCATCTGTATATCTATGTAATG 30356
Db 30043 GGCTTGTCACTTTTGTCTCATGGAGAGTGGCTACTGCATCCATGTTATATCTATGTAATG 30102
Qy 30357 TTGACCTGGAGAGCATCACTTGACTTTTCCAGCAGAGAAATACAGCTGATGACAGCTG 30416
Db 30103 TTGACCTGGAGAGCATCACTTGACTTTTCCAGCAGAGAAATACAGCTGATGACAGCTG 30162
Qy 30417 CTGCTGAGAAAAATGGATATTTTCTGAATTCAGTCTTACGTGGAAAAACAGCTGACTAGTTT 30476
Db 30163 CTGCTGAGAAAAATGGATATTTTCTGAATTCAGTCTTACGTGGAAAAACAGCTGACTAGTTT 30222
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chromosome 10q25.2, complete sequence.
ACCESSION AF042484
VERSION AF042484.1 GI:4205782
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Barry,A.B., Howman,E.V., Cancilla,M.R., Saffery,R. and Choo,K.H.
TITLE Sequence analysis of an 80 kb human neocentromere
JOURNAL Hum. Mol. Genet. 8 (2), 217-227 (1999)
MEDLINE 99135901
PUBMED 9931329
REFERENCE 2 (bases 1 to 80155)
Barry,A.B., Howman,E.V., Cancilla,M.R., Saffery,R. and Choo,A.
Direct Submission
Submitted (13-JAN-1998) Chromosome Research Unit, The Murdoch
Institute, 10th Floor, Royal Childrens Hospital, Flemington Rd.,
Parkville, Melbourne, Victoria 3052, Australia
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QY 6351 GGTGAACCTAAGTAAGCAGAGGCTGCTGTCTAGTAGGGGTAGGCATCATCCAGTCTGTTG 6410
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Db |||||

Db 6471 GAGACATCTATCTCTGCCCTTGGCACTCTCTGTTCTCAGGGGTTTCAGACCTCGAATCTCTGG 6530
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Db |||||

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Qy	10147	ATGCAGTACAGGATGAAATTTTCAGCTGAGTATCTAGAGAAATCCCGATAGTGAATC	10206	Db	10851	TGGAGCTCTAAGTGTCTTTCAGAAATAGCAAAACACTAGTCTTTCTTTCTTTTCTTTT	10909
Db	9771	ATGCAGTACAGGATGAAATTTTCAGCTGAGTATCTAGAGAAATCCCGATAGTGAATC	9830	Qy	11287	TTTTTTTGGAGACAGAGTCTTTGGTCTGTCTGCCCCAGGCTGGAGTGCATAGCAGATCTC	11346
Qy	10207	TGTTAAGCTCTCTGAGTGTGGCTTTTCCCTGGAGAGCAATAGAAAATTCAGTCTTAA	10266	Db	10910	TTTTTTTGGAGACAGAGTCTTTGGTCTGTCTGCCCCAGGCTGGAGTGCATAGCAGATCTC	10969
Db	9831	TGTTAAGCTCTCTGAGTGTGGCTTTTCCCTGGAGAGCAATAGAAAATTCAGTCTTAA	9890	Qy	11347	CGCTCACTGAACTCTGCTCCCGGTTCAAGCGACTCTCTCTGCTCAGCTCTCCGAGTAG	11406
Qy	10267	CGATTTTAAAGTTCTTGGAACTAGTATTAGATGATCTTAGAGAAATTTATTAAAT	10326	Db	10970	CGCTCACTGAACTCTGCTCCCGGTTCAAGCGACTCTCTCTGCTCAGCTCTCCGAGTAG	11029
Db	9891	CGATTTTAAAGTTCTTGGAACTAGTATTAGATGATCTTAGAGAAATTTATTAAAT	9950	Qy	11407	CTGGATTACAGGTGCCCCACCAACGCGCCAGCTAAATTTTCTATTTTATAGATGAGA	11466
Qy	10327	TGTTAAGCTCTCTGAGTGTGGCTTTTCCCTGGAGAGCAATAGAAAATTCAGTCTTAA	10386	Db	11030	CTGGATTACAGGTGCCCCACCAACGCGCCAGCTAAATTTTCTATTTTATAGATGAGA	11089
Db	9951	TGTTAAGCTCTCTGAGTGTGGCTTTTCCCTGGAGAGCAATAGAAAATTCAGTCTTAA	10010	Qy	11467	GGTTTCAACGCTTGGCCAGAGCTGTCTCAAACTCTCTGGCTCAAGTATCCGCTGCT	11526
Qy	10387	ATACCTGAAATATAAGCATAGATATGATGTAGGAGATTTGCTTTAAATACCAGTA	10446	Db	11090	GGTTTCAACGCTTGGCCAGAGCTGTCTCAAACTCTCTGGCTCAAGTATCCGCTGCT	11149
Db	10011	ATACCTGAAATATAAGCATAGATATGATGTAGGAGATTTGCTTTAAATACCAGTA	10070	Qy	11527	TGGCTCCCAAAGTCTGGGATTACAGGTGTGAGCCACCAACCCAGCTGCAAAACCTTA	11586
Qy	10447	AGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10506	Db	11150	TGGCTCCCAAAGTCTGGGATTACAGGTGTGAGCCACCAACCCAGCTGCAAAACCTTA	11209
Db	10071	AGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10130	Qy	11587	TTTTTTTGAATGGAGAAACACTTTCCCTTATTTATTTAGTGTGGAGCAAGAGAGG	11646
Qy	10507	GAAGGAGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10566	Db	11210	TTTTTTTGAATGGAGAAACACTTTCCCTTATTTATTTAGTGTGGAGCAAGAGAGG	11269
Db	10131	GAAGGAGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10190	Qy	11647	GGTAATTCATTAAGTGAATAATTTCCAAATCCAGAAACATCGATAAAGCAGAGCTTAA	11706
Qy	10567	CATGCTTATATCCAGCATTTAGGAGGCAAGTGTGGAGGATCACTTAATTAAGCCAG	10626	Db	11270	GGTAATTCATTAAGTGAATAATTTCCAAATCCAGAAACATCGATAAAGCAGAGCTTAA	11329
Db	10191	CATGCTTATATCCAGCATTTAGGAGGCAAGTGTGGAGGATCACTTAATTAAGCCAG	10250	Qy	11707	TTTTTTTGAAGAAATTTTAAACTATCTTTTGGAGCTCTTTAGGAGACCTTAC	11766
Qy	10627	GAGTTCAAGCTGAGTACGCTGATTTGGCCCACTGCACTCCAGCTGGGTGGGAGAGT	10686	Db	11330	TTTTTTTGAAGAAATTTTAAACTATCTTTTGGAGCTCTTTAGGAGACCTTAC	11389
Db	10251	GAGTTCAAGCTGAGTACGCTGATTTGGCCCACTGCACTCCAGCTGGGTGGGAGAGT	10310	Qy	11767	GTCTTGGCTTGAATTTGAGAGTGGGAAATCCAGGGA-GTTTTGGAATGATGCTTAT	11825
Qy	10687	GAAGCCCTGTCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10746	Db	11390	GTCTTGGCTTGAATTTGAGAGTGGGAAATCCAGGAGGTTTTGGAATGATGCTTAT	11449
Db	10311	GAAGCCCTGTCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10370	Qy	11826	GTCTGCTTTTGTGTTAGAGAAATATAAATATTTTATCTAGGTTTTGCTGATGGAG	11885
Qy	10747	TGSCAAGATTTGGTAAATGTTGAACCTGAAGGAGTAAATATGATGAGTTCACCTTCT	10806	Db	11450	GTCTGCTTTTGTGTTAGAGAAATATAAATATTTTATCTAGGTTTTGCTGATGGAG	11509
Db	10371	TGSCAAGATTTGGTAAATGTTGAACCTGAAGGAGTAAATATGATGAGTTCACCTTCT	10430	Qy	11886	TCAGCATGAACAAACCACTGTTGAGAGCTGTAATTTCTGAAATTTCTGCAAGAGTC	11945
Qy	10807	TCAGTCTTCTTATGATGTTTCCCACTTTCATATTAACAAATTTAAATATTTTCTC	10866	Db	11510	TCAGCATGAACAAACCACTGTTGAGAGCTGTAATTTCTGAAATTTCTGCAAGAGTC	11569
Db	10431	TCAGTCTTCTTATGATGTTTCCCACTTTCATATTAACAAATTTAAATATTTTCTC	10490	Qy	11946	ACATCTAGGCCAGCAAAATGGCAGTAAGAGTGAAGTGGATTTAGCTCAGTGTAAAGATGAA	12005
Qy	10867	TGATCAAAACTTAGTACAGTATTAATCCCTGGGCTTCCCTGACTAGAAAGCTTATAC	10926	Db	11570	ACATCTAGGCCAGCAAAATGGCAGTAAGAGTGAAGTGGATTTAGCTCAGTGTAAAGATGAA	11629
Db	10491	TGATCAAAACTTAGTACAGTATTAATCCCTGGGCTTCCCTGACTAGAAAGCTTATAC	10550	Qy	12006	CTCCAGAACCACTGGCTCTGACTGAAGTGAAGCGGAGCCGCTTGTGGGAAAGCTGGC	12065
Qy	10927	CACATGGGAGAGTCTGGCCGACAGGAGCAAGTGTGGTTTCAACATCTTCTGCTGT	10986	Db	11630	CTCCAGAACCACTGGCTCTGACTGAAGTGAAGCGGAGCCGCTTGTGGGAAAGCTGGC	11689
Db	10551	CACATGGGAGAGTCTGGCCGACAGGAGCAAGTGTGGTTTCAACATCTTCTGCTGT	10610	Qy	12066	TGGAGTCTCTCTCATAGCAGGCAATCTTTTCTCCAGCCGCTCACTGTGTGTTTGGG	12125
Qy	10987	AATGTGTCTGGGCTGAAGGCTTCTTAAAGTGTGATAGAAATCCAGGAACTTCT	11046	Db	11690	TGGAGTCTCTCTCATAGCAGGCAATCTTTTCTCCAGCCGCTCACTGTGTGTTTGGG	11749
Db	10611	AATGTGTCTGGGCTGAAGGCTTCTTAAAGTGTGATAGAAATCCAGGAACTTCT	10670	Qy	12126	CCCAGGTAAAGCTCTGCTGGCTCTAGGCTGTAAACCCCAACCATCTCTGCTGCTGCT	12185
Qy	11047	TAGAACTGACAGACTATCAGGTAACCTGACAGGAGTGAAGTACTAAGTGAAGAGCAG	11106	Db	11750	CCCAGGTAAAGCTCTGCTGGCTCTAGGCTGTAAACCCCAACCATCTCTGCTGCTGCT	11809
Db	10671	TAGAACTGACAGACTATCAGGTAACCTGACAGGAGTGAAGTACTAAGTGAAGAGCAG	10730	Qy	12186	CCAGAGTCAATTTCTGAAGCACAACCTGGATGTCAATCCCTTCTGAACTCTTAGCACC	12245
Qy	11107	AGGCGAGAGTCTGATATGACAGCTGACGCCCTTCTTCTGTCCTCATTCGTGGA	11166	Db	11810	CCAGAGTCAATTTCTGAAGCACAACCTGGATGTCAATCCCTTCTGAACTCTTAGCACC	11869
Db	10731	AGGCGAGAGTCTGATATGACAGCTGACGCCCTTCTTCTGTCCTCATTCGTGGA	10790	Qy	12246	TACAGGAGTCCATCTTGTGCCCCACATACCTCAACGTPAGACATTCCTTAATGAAGAT	12305
Qy	11167	AAATTGAGTGGAGTCAATTTTGAAGTGGAGTCTAAGTAGCTCCACTTGTAGACATTTAG	11226	Db	11870	TACAGGAGTCCATCTTGTGCCCCACATACCTCAACGTPAGACATTCCTTAATGAAGAT	11929
Db	10791	AAATTGAGTGGAGTCAATTTTGAAGTGGAGTCTAAGTAGCTCCACTTGTAGACATTTAG	10850	Qy	12306	TGATTTGAATTTTGAATTAACCTGAGTGGCTCCCACTCTTCTAGTTGCTCTCTGCTGCT	12365
Qy	11227	TGAGCTCTAAGTGTCTTCAGAAATAGCAAAACACTAGTCTTTCTTTTCTTTTCTTTT	11286				

QY	18882	TGCACATTCCTCCAGCTGCTGCTCGGTGGTGCACAGTGCATTAATGTGGCGCTTCCTG	18941	Db	19607	TGTATGGATATAGCTAAAGGGTTGGCCCTTTATGTTTCTATTTCTTCAAAACCTGGTAGA	19666
Db	18527	TGCACATTCCTCCAGCTGCTGCTCGGTGGTGCACAGTGCATTAATGTGGCGCTTCCTG	18586	QY	20021	ATAGATATGCTGTTGTTCCCTTTAAATAATGTCACAAATGTCATTTATGATGCTGCTGATATA	20080
QY	18942	GTGCAAACTGCTCACTTAGCTCCGCTCTGCTGGCACAGCAGAGAAATCGAATA	19001	Db	19667	ATAGATATGCTGTTGTTCCCTTTAAATAATGTCACAAATGTCATTTATGATGCTGCTGATATA	19726
Db	18587	GTGCAAACTGCTCACTTAGCTCCGCTCTGCTGGCACAGCAGAGAAATCGAATA	18646	QY	20081	GTAACCTCACAGATCATGCTCCATGAAATGCTTCAGAACCCCAATATAAGGAGATTTTTTA	20140
QY	19002	TGTTGGATTTCAAAGGTAAACAAGAGCTGGAAAACAATCTAGCCGAGTCTGAGAGTT	19061	Db	19727	GTAACCTCACAGATCATGCTCCATGAAATGCTTCAGAACCCCAATATAAGGAGATTTTTTA	19786
Db	18647	TGTTGGATTTCAAAGGTAAACAAGAGCTGGAAAACAATCTAGCCGAGTCTGAGAGTT	18706	QY	20141	GCCATGTGTGACAAAGAGAGGCCATTTCAGTGTGAAATGTTTCAGAGAATGATTTGAT	20200
QY	19062	TCAGCGGAGTCTGGTGGAGCTTGTGTTTTCACCTGACAGCTGAAAATGAGCCGAGCTT	19121	Db	19787	GCCATGTGTGACAAAGAGAGGCCATTTCAGTGTGAAATGTTTCAGAGAATGATTTGAT	19846
Db	18707	TCAGCGGAGTCTGGTGGAGCTTGTGTTTTCACCTGACAGCTGAAAATGAGCCGAGCTT	18766	QY	20201	TATGTTTTCTCAGATCTTTTTTATTTTTTATTTTTTGAACAGAGTCTCATTGTCACCC	20260
QY	19122	CAGTGAAGCTTGTGTTTCTTCCCTCCCTCAAGGTTACCCACAATCTCAGTCTCTCAGGAA	19181	Db	19847	TATGTTTTCTCAGATCTTTTTTATTTTTTATTTTTTGAACAGAGTCTCATTGTCACCC	19906
Db	18767	CAGTGAAGCTTGTGTTTCTTCCCTCCCTCAAGGTTACCCACAATCTCAGTCTCTCAGGAA	18826	QY	20261	CAGGCTGAGTACAGTGGCTGTGCTCGGCTCTCTGAACTCTGCTCCAGGTTCAA	20320
QY	19182	AGCCAAAATAATGAAATTTAGGGTTTAGGATTTGGTTCTTTTATCTATTACAGGATTTGAT	19241	Db	19907	CAGGCTGAGTACAGTGGCTGTGCTCGGCTCTCTGAACTCTGCTCCAGGTTCAA	19966
Db	18827	AGCCAAAATAATGAAATTTAGGGTTTAGGATTTGGTTCTTTTATCTATTACAGGATTTGAT	18886	QY	20321	GCGATTCCTGTCAGCTTCCCGAATAGCTGGGATTCAGCGCGATGCACACCATGGCT	20380
QY	19242	AATATGTTCTCTCCACAGATGTTCTGCTGTGTAACAATCTCATTCTCTGACACTACTGCA	19301	Db	19967	GCGATTCCTGTCAGCTTCCCGAATAGCTGGGATTCAGCGCGATGCACACCATGGCT	20026
Db	18887	AATATGTTCTCTCCACAGATGTTCTGCTGTGTAACAATCTCATTCTCTGACACTACTGCA	18946	QY	20381	AATTTTTGTATTTTATGATGAGACAGAGTTTCGCCATGTTGACACAGGCTTGCCTTGAAC	20440
QY	19302	TATGCAAGGATGTTACTACCAAGTAAACAAGAAATGCTGCCAAATCCAAATCCCTG	19361	Db	20027	AATTTTTGTATTTTATGATGAGACAGAGTTTCGCCATGTTGACACAGGCTTGCCTTGAAC	20086
Db	18947	TATGCAAGGATGTTACTACCAAGTAAACAAGAAATGCTGCCAAATCCAAATCCCTG	19006	QY	20441	CCTGACCTCAGTGCATCCACCCACTCAGCTCCCGAAGCAGCTGGGATTCAGGCATGAG	20500
QY	19362	AACGTAGTACAGAAATCAGAAATATAAGGGATTCACAGAGCTGCTACGATGTG	19421	Db	20087	CCTGACCTCAGTGCATCCACCCACTCAGCTCCCGAAGCAGCTGGGATTCAGGCATGAG	20146
Db	19007	AACGTAGTACAGAAATCAGAAATATAAGGGATTCACAGAGCTGCTACGATGTG	19066	QY	20501	CCACGCTGCCAGCCTGTTTTCTCAGATCTCTGTA- TTTGTTTCTGAAAGCTTCAATTTCTA	20559
QY	19422	CCAGTGGTACAGATCTGTTGCTATCATAGCAGGCTGCTGCTCTAGCAATCTGCTCACT	19481	Db	20147	CCACGCTGCCAGCCTGTTTTCTCAGATCTCTGTA- TTTGTTTCTGAAAGCTTCAATTTCTA	20206
Db	19067	CCAGTGGTACAGATCTGTTGCTATCATAGCAGGCTGCTGCTCTAGCAATCTGCTCACT	19126	QY	20560	TCCTTCTTATTCATTTTGGAGTAGTACACCTAGTAAAGTTTAAACAATCAATATCTT	20619
QY	19482	GCTTCATTTCTGCTGCTTTTAAATACTGCTTTTCTCAGCTCAATTTGGCTTCTTCC	19541	Db	20207	TCCTTCTTATTCATTTTGGAGTAGTACACCTAGTAAAGTTTAAACAATCAATATCTT	20266
Db	19127	GCTTCATTTCTGCTGCTTTTAAATACTGCTTTTCTCAGCTCAATTTGGCTTCTTCC	19186	QY	20620	TGGAATAATTCCTGGTTCCCTTTCTTATTCCTACAAAATATGTTTCAGTATAGCTGATGT	20679
QY	19542	CTCTGGCAGTCAAGTCTTCTTGGGTCAACAGCAAAATGATTTTAAAGATCACTGGTAC	19601	Db	20267	TGGAATAATTCCTGGTTCCCTTTCTTATTCCTACAAAATATGTTTCAGTATAGCTGATGT	20326
Db	19187	CTCTGGCAGTCAAGTCTTCTTGGGTCAACAGCAAAATGATTTTAAAGATCACTGGTAC	19246	QY	20680	ATGTTTCTTCAAATATTCATTTCTCTATCTCAGAAATTTATCTCATGCCCTTAATGTTAT	20739
QY	19602	TCAAAGAGCTACAAGACATGGGCATCCACTCTCTTGGAAAAACAATTTATG	19661	Db	20327	ATGTTTCTTCAAATATTCATTTCTCTATCTCAGAAATTTATCTCATGCCCTTAATGTTAT	20386
Db	19247	TCAAAGAGCTACAAGACATGGGCATCCACTCTCTTGGAAAAACAATTTATG	19306	QY	20740	TGAATAGTCTTCACTTCTTGTCTCAGTTTCTGTTCTCTTATTTCTCACTCTTAAGCTAAAG	20799
QY	19662	GAAAGCAAGGTTGCCATAGTCCCTCTGAGGTTGTTGCTCAGCAAGGCCCAAGCTTGG	19721	Db	20387	TGAATAGTCTTCACTTCTTGTCTCAGTTTCTGTTCTCTTATTTCTCACTCTTAAGCTAAAT	20446
Db	19307	GAAAGCAAGGTTGCCATAGTCCCTCTGAGGTTGTTGCTCAGCAAGGCCCAAGCTTGG	19366	QY	20800	TGGCTATTAGAAATAAGAGCTTGAACAGATTTCTTCTCCAAATATGTTTATCTTTTGAC	20859
QY	19722	TGCTTCAAACATGAAATTAGAGAGCTTCAGAACAGATCCACTTTTCAATGGCTCACC	19781	Db	20447	TGGCTATTAGAAATAAGAGCTTGAACAGATTTCTTCTCCAAATATGTTTATCTTTTGAC	20506
Db	19367	TGCTTCAAACATGAAATTAGAGAGCTTCAGAACAGATCCACTTTTCAATGGCTCACC	19426	QY	20860	TGCATGCCAGTGCACAACTGTTACTGTTTGTGTTTCTTCAATATTCACAGAACATGC	20919
QY	19782	CAACTGGATTAAGAACAAATGGCAATATCTCAATGACACCTTTT-TCAGGTGGAGTGT	19840	Db	20507	TGCATGCCAGTGCACAACTGTTACTGTTTGTGTTTCTTCAATATTCACAGAACATGC	20566
Db	19427	CAACTGGATTAAGAACAAATGGCAATATCTCAATGACACCTTTTCTCAGGTGGAGTGT	19486	QY	20920	TGACTCTCTCTTCTGAAAGCAATGGCCCAAGCAGCAGATTGTTAGTAGTATGATGACCA	20979
QY	19841	AGATGCTGGAATGGGTACAGACATTCGCCAACCAAACTTTGAAAAAGGCTGGAAGCTC	19900	Db	20567	TGACTCTCTCTTCTGAAAGCAATGGCCCAAGCAGCAGATTGTTAGTAGTATGATGACCA	20626
Db	19487	AGATGCTGGAATGGGTACAGACATTCGCCAACCAAACTTTGAAAAAGGCTGGAAGCTC	19546	QY	20980	ACAGGACATGGGTGCTAGCAAAAACCTAGAGGAAGAGGACCTTCCCTTAGCAATGGGT	21039
QY	19901	TGACTGGGACCTTAATATGAAAAAGTTGATAGGCTCTTCTATGCAAGATATGAACCCCG	19960	Db	20627	ACAGGACATGGGTGCTAGCAAAAACCTAGAGGAAGAGGACCTTCCCTTAGCAATGGGT	20686
Db	19547	TGACTGGGACCTTAATATGAAAAAGTTAATAGGCTCTTCTATGCAAGATATGAACCCCG	19606	QY	21040	GATATGGTCCCTGGACTTAGACTCCAAAGGCTCTGAGGTGAAACACACATCGTCCATAC	21099
QY	19961	TGTAATGATATAGCTAAAGGTTGGCTTTTATGTTTCTTATCTCTTCAACAACTGGTAGA	20020				

Db 25067 CTTTCTGAGAGCCTGAGAACTTTAGCATAATTTTCCTT-GAAATTACAGCTCAATATTTT 25125
QY 25479 CAGCACTTTATACAAACAGCCTAAAGTTAGCTTGCCCAATACAGTGTTTCAAGGTAATA 25538
Db 25126 CAGCACTTTATACAAACAGCCTAAAGTTAGCTTGCCCAATACAGTGTTTCAAGGTAATA 25185
QY 25539 AACTCTTTTCTTTCTGTCGCGATTGAAAGAACTGCTGTAGCTTACGCTCCTGCGAGATGATG 25598
Db 25186 AACTCTTTTCTTTCTGTCGCGATTGAAAGAACTGCTGTAGCTTACGCTCCTGCGAGATGATG 25245
QY 25599 AACTGGGTACACAGAGCAATTTTCCAGGTAAGCAATATTTTCGTCGCACTTTCTTAAGCTG 25658
Db 25246 AACTGGGTACACAGAGCAATTTTCCAGGTAAGCAATATTTTCGTCGCACTTTCTTAAGCTG 25305
QY 25659 CAGCCTTATATGCAATAATGTGTCATTTTACAGACTTTATGTTTCAAGCTTTTTCAGGCACTCTG 25718
Db 25306 CAGCCTTATATGCAATAATGTGTCATTTTACAGACTTTATGTTTCAAGCTTTTTCAGGCACTCTG 25365
QY 25719 TTTTCACTAACATATCCTTCAACTTTGATAAGTACTGCTTTTAACTCAACTCAGAAAAATTT 25778
Db 25366 TTTTCACTAACATAT-CTTCAACTTTGATAAGTACTGCTTTTAACT-ACCTCAGAAAAATTT 25423
QY 25779 AACTTCAGTAATTTTTTTTTCACCATCAGTTTTTTTTTCTGCTGACTTTTCTCTCTTTTCT 25838
Db 25424 AACTTCAGTAATTTTTTTTTCACCATCAGTTTTTTTTTCTGCTGACTTTTCTCTCTTTTCT 25483
QY 25839 GTTTGCCAGAAACATGCTCAGGATCTCTCAGGCTTTTAAAAAATGAAAAATGTTTCTCT 25898
Db 25484 GTTTGCCAGAAACATGCTCAGGATCTCTCAGGCTTTTAAAAAATGAAAAATGTTTCTCT 25543
QY 25899 GCAATCTAGTACTCTCTGATCTCTGTTTCTGTTTATCGCTGGAATCTTCAAGAGCTTG 25958
Db 25544 GCAATCTAGTACTCTCTGATCTCTGTTTCTGTTTATCGCTGGAATCTTCAAGAGCTTG 25603
QY 25959 GTGTATTAGTCTTTTTTTCATGCTGTGATAAGATATACCTGAGAGCTGGATTAATTTATAA 26018
Db 25604 GTGTATTAGTCTTTTTTTCATGCTGTGATAAGATATACCTGAGAGCTGGATTAATTTATAA 25663
QY 26019 AGAAAAAGAGTTTAAAGACTCAGTTTCCAGCTGCTGAGAGAGCTTCAAAATCATGG 26078
Db 25664 AGAAAAAGAGTTTAAAGACTCAGTTTCCAGCTGCTGAGAGAGCTTCAAAATCATGG 25723
QY 26079 TGAAGGCAAAAGGCAATGCTTACATGCGAGAGAGAGAGAGATGAGAACCAAGGGAT 26138
Db 25724 TGAAGGCAAAAGGCAATGCTTACATGCGAGAGAGAGAGATGAGAACCAAGGGAT 25783
QY 26139 TTCCCTTTATAAAACCAATCAGATCTTTGAGAGCTTTATTCACACCAAGAGACATATGG 26198
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Db 25844 GGTAAACCGCCCGCATGATTTCAATTTATCTCCACCGGGCCCTCCACACACGTTGGGAA 25903
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Db 25904 TTATGGGAGTACAATTTCAAGATGACATTTGGGTGGGACATGGGCCAAACCATATACCT 25963
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Db 25964 GGCTATAGCAATTTATTTCTATTTCTCCCATCTTTTCTCCATCTTCTCAACCGGTGACAA 26023
QY 26379 GACTCTTTTTTTTTTTTCTACTCGAACTGCTTTTTGAGGGTACGTGATAAGTCCAA 26438
Db 26024 GACTCTTTTTTTTTTTTCTACTCGAACTGCTTTTTGAGGGTACGTGATAAGTCCAA 26083
QY 26439 AATCTGTACCTTTTCTGAACTTCCGTTCTTCTTATGCTTTTGGAGCAATGACGTGTG 26498
Db 26084 AATCTGTACCTTTTCTGAACTTCCGTTCTTCTTATGCTTTTGGAGCAATGACGTGTG 26143
QY 26499 TGGTTGCCCTCTCTTTAAAGTGTCTCTCACTTGGTTTTT-ATGACTAATGATGATTT 26554
Db 26144 TGGTTGCCCTCTCTTTAAAGTGTCTCTCACTTGGTTTTTATGACTAATGATGATTT 26203

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QY 26615 AATGTCCTTGTTCAGAGAACTGCTGCTGCTTGTGACTTCTCTATGCTGCTGCTGCTGCT 26674
Db 26264 AATGTCCTTGTTCAGAGAACTGCTGCTGCTTGTGACTTCTCTATGCTGCTGCTGCTGCT 26323
QY 26675 AACTCATGGGTCTTTTATTAATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 26734
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QY 26735 TTTCACTCTCCCAATTTTCAAAATGCTCCAGAGAACTTTCCAAATGAGTATCTCTCAATGTA 26794
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QY 26795 TTTAACTGCTAAATATTAACACATAATCTTTCCCATCAAAATCGTTTCTCTTAAAGTT 26854
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QY 26855 TTTGTTATTTTCTTATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 26914
Db 26504 TTTGTTATTTTCTTATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 26563
QY 26915 TTTTCTGACCAATACCTCTCTTTTCTGCTCCCATATCAATTTAGTAGCAAGTGTATCAATG 26974
Db 26564 TTTTCTGACCAATACCTCTCTTTTCTGCTCCCATATCAATTTAGTAGCAAGTGTATCAATG 26623
QY 26975 ATTTACTTGACAAATATCTTTTCTTATTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 27034
Db 26624 ATTTACTTGACAAATATCTTTTCTTATTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 26683
QY 27035 GAGTTGCCCTTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 27094
Db 26684 GAGTTGCCCTTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 26743
QY 27095 AATATTTGAAAGAAAAAGAGCTCTATCTGAGTATGAAAAATTTTATTTCTGCTGCTGCTGCT 27154
Db 26744 AATATTTGAAAGAAAAAGAGCTCTATCTGAGTATGAAAAATTTTATTTCTGCTGCTGCTGCT 26803
QY 27155 TCCCTAAACAAATACAGTATTAACAACTACAGCTTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 27214
Db 26804 TCCCTAAACAAATACAGTATTAACAACTACAGCTTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 26863
QY 27215 TCTAGAAATGATTTCAAGTACACATTTATATAAGGAGCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 27274
Db 26864 TCTAGAAATGATTTCAAGTACACATTTATATAAGGAGCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 26923
QY 27275 GTATTTGTGGGCACTACTGGGACCAATTTCCCATGAGTATACAGAGGACCACTATATTTA 27334
Db 26924 GTATTTGTGGGCACTACTGGGACCAATTTCCCATGAGTATACAGAGGACCACTATATTTA 26983
QY 27335 CTGAGTCTTACTTAAATACAGTGTGGCAATGTTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 27394
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QY 27395 TAGTTTGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 27454
Db 27044 TAGTTTGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 27103
QY 27455 ATTCTATTTCTTAAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 27514
Db 27104 ATTCTATTTCTTAAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 27163
QY 27515 CTCACTTTGTAATCCAGCAATTTTGGGAGGCGCAAGGGGGGTGATFCACTTGAAGTFCAG 27574
Db 27164 CTCACTTTGTAATCCAGCAATTTTGGGAGGCGCAAGGGGGGTGATFCACTTGAAGTFCAG 27223
QY 27575 GAGTTCCAGACAGCTTGGCGCAACATGCGCAACCTGCTCTACAAAAAGTATATAAG 27634
Db 27224 GAGTTCCAGACAGCTTGGCGCAACATGCGCAACCTGCTCTACAAAAAGTATATAAG 27283

QY	27635	TTAAACAGGTGCTGAGCAATTTGCTGTGTGCCAGTACTCAGGAGGCTGAGGCAGGAA	27694	Db	28363	CGGCAAAATGATGCTTAACACCTTTCTATCTTTATAGTGTCTTGTGTGT	28422
Db	27284	TTAAACAGGTGCTGAGCAATTTGCTGTGTGCCAGTACTCAGGAGGCTGAGGCAGGAG	27343	QY	28774	TGCTATAAGGAATACCTGAGGCTGGGGAATTTATTTAAAAAAGAGGTTTATTTGGCTCA	28833
QY	27695	AATCACATTTAATCTGGGAGGTGGAGTTTGAGTGGCCAGATCTCTCCACTGCATCCCA	27754	Db	28423	TGCTATAAGGAATACCTGAGGCTGGGGAATTTATTTAAAAAAGAGGTTTATTTGGCTCA	28482
Db	27344	AATCGCTTTAATCTGGGAGGTGGAGTTTGAGTGGCCAGATCTCTCCACTGCATCCCA	27403	QY	28834	CAGTTCTGCAGCTATATAAGGAAGCATAGTGTCCAGATCTGCTTCAGGTGAGGGCTTCAGG	28893
QY	27755	GCCTGGGTGACACAGCAAGACTCTATCTCAAAACAAATAAACAACAACAACAACAACA	27814	Db	28483	CAGTTCTGCAGCTATATAAGGAAGCATAGTGTCCAGATCTGCTTCAGGTGAGGGCTTCAGG	28542
Db	27404	GCCTGGGTGACACAGCAAGACTCTATCTCAAAACAAATAAACAACAACAACAACAACA	27463	QY	28894	AAGTTTCCACCATGTTAGAAAGGCAAGGGGAGCAGGCATCACATATCAAGAGAGGAGGA	28953
QY	27815	TTTAATGGCTGCACCTTGCTGTGAAATAATGCAATTTCTTGGCCAGATGTGGTGGCTCAAA	27874	Db	28543	AAGTTTCCACCATGTTAGAAAGGCAAGGGGAGCAGGCATCACATATCAAGAGAGGAGGA	28602
Db	27464	TTTAATGGCTGCACCTTGCTGTGAAATAATGCAATTTCTTGGCCAGATGTGGTGGCTCAAA	27523	QY	28954	AAAAAGGAAGGAAGAAAGGAGGGTGCATTTCTTTCAACAATCAGTTCTTGTGGGAAC	29013
QY	27875	CCTGTAAATCCCAACATCTTGGGAAGCTTAAGGCCAGGAGTTTCGAGAGAGTGGATATAT	27934	Db	28603	AAAAAGGAAGGAAGAAAGGAGGGTGCATTTCTTTCAACAATCAGTTCTTGTGGGAAC	28662
Db	27524	CCTGTAAATCCCAACATCTTGGGAAGCTTAAGGCCAGGAGTTTCGAGAGAGTGGATATAT	27583	QY	29014	TAAATGGGCAAGAGAGGCTGGGCACGCTGGCTCATCGCTGTATCCAGAGCCCTTTGGGAGAC	29073
QY	27935	AGGAAGACAAATCTCTPACAAAAAATAATCCACAAATTTAGTCAGGCTTATTTGTTATGCG	27994	Db	28663	TAAATGGGCAAGAGAGGCTGGGCACGCTGGCTCATCGCTGTATCCAGAGCCCTTTGGGAGAC	28722
Db	27584	AGGAAGACAAATCTCTPACAAAAAATAATCCACAAATTTAGTCAGGCTTATTTGTTATGCG	27643	QY	29074	CAAGTGGGTGGATCACTGAAGTCAAGAGCCTGAGACAGCCTGGCCCAATGTGGTGAAT	29133
QY	27995	CTGTAGTCCAGGACTCAGAGGCTGAGGAGGATTCCTCAAGCCAGAGTTCAAGGC	28054	Db	28723	CAAGTGGGTGGATCACTGAAGTCAAGAGCCTGAGAGCCTGAGACAGCCTGGCCCAATGTGGTGAAT	28782
Db	27644	CTGTAGTCCAGGACTCAGAGGCTGAGGAGGATTCCTCAAGCCAGAGTTCAAGGC	27703	QY	29134	CTCCGTCTCTACTAAAAATACAAAAAT-----TAGCTGGGCTGGTGGGCTGTACCTGT	29187
QY	28055	TTCCGTGAGCTATATGGCAACCTGCACCTCCATCTTGGGTGACAGAGCAAGTCCATATC	28114	Db	28783	CTCCGTCTCTACTAAAAATACAAAAAT-----TAGCTGGGCTGGTGGGCTGTACCTGT	28842
Db	27704	TTCCGTGAGCTATATGGCAACCTGCACCTCCATCTTGGGTGACAGAGCAAGTCCATATC	27763	QY	29188	AGTCCAGATACTCAGAGGCTGAGTGAAGTAAATCACTTGAAACCCGGAAGACAGAGTT	29247
QY	28115	TCCTGGGAAAAAATAAAGAGGCAATTTCTTAGGAGGTTCTTCTGTAGAGTCCTA	28174	Db	28843	AGTCCAGATACTCAGAGGCTGAGTGAAGTAAATCACTTGAAACCCGGAAGACAGAGTT	28902
Db	27764	TCCTGGGAAAAAATAAAGAGGCAATTTCTTAGGAGGTTCTTCTGTAGAGTCCTA	27822	QY	29248	GCAGTGGCTTGTGCCACTGCCCTCCAGCCGGGCAACAGAGTGAAGAGGCTCTCAAAAA	29307
QY	28175	AGGTTTCCATGGAACCTTTAAAGCATCAGAGTATGTGAGTGCATGGAGCAAGCATT	28234	Db	28903	GCAGTGGCTTGTGCCACTGCCCTCCAGCCGGGCAACAGAGTGAAGAGGCTCTCAAAAA	28962
Db	27823	AGGTTTCCATGGAACCTTTAAAGCATCAGAGTATGTGAGTGCATGGAGCAAGCATT	27882	QY	29308	TTTTAAAAATTTAAAAATATAGAGCAAGAAACCAAGTTTATCAGGAGGATCCAC	29367
QY	28235	TAGCCAGAGAGTTGTGCTCCCATTCGATATTAATTTTAAAAAACAAGCTATAAAAA	28294	Db	28963	TTTTAAAAATTTAAAAATATAGAGCAAGAAACCAAGTTTATCAGGAGGATCCAC	29022
Db	27883	TAGCCAGAGAGTTGTGCTCCCATTCGATATTAATTTTAAAAAACAAGCTATAAAAA	27942	QY	29368	CCCCAATGACTCAATACCTCCACAGGCTCCTCACTCCAACTGCGGATCAATTTCCG	29427
QY	28295	AAGTTGAAACTACTAGCTTAGCATCAGCTGCAATTTAATGCTGCTGTAATCAACCT	28354	Db	29023	CCCCAATGACTCAATACCTCCACAGGCTCCTCACTCCAACTGCGGATCAATTTCCG	29082
Db	27943	AAGTTGAAACTACTAGCTTAGCATCAGCTGCAATTTAATGCTGCTGTAATCAACCT	28002	QY	29428	TATCAGATTTTGGAGGAGCAAAATATCCAACTATATCACATAGTAATGAACATAGTACCT	29487
QY	28355	TAAATGACTTTTATGAGGAGTTATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG	28414	Db	29083	TATCAGATTTTGGAGGAGCAAAATATCCAACTATATCACATAGTAATGAACATAGTACCT	29142
Db	28003	TAAATGACTTTTATGAGGAGTTATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG	28062	QY	29488	TATCCTATAGAAAGCAATGGCTAGACAACTGTGTGAATGGCTAAACCAATCTGCTTCTAT	29547
QY	28415	AATTAGACTAATAGTTGTATCATAGTGAATCAAGTTTGGCAATCTTCCATGCTTGTGT	28474	Db	29143	TATCCTATAGAAAGCAATGGCTAGACAACTGTGTGAATGGCTAAACCAATCTGCTTCTAT	29202
Db	28063	AATTAGACTAATAGTTGTATCATAGTGAATCAAGTTTGGCAATCTTCCATGCTTGTGT	28122	QY	29548	GGTCTCCCTCTAGAGGGGCTCAGTATGAGTTTCTCAAAAGGAGAAAAAATGATATA	29607
QY	28475	CACACATTAACCTTTCTGGAATGCTCTGCTACTCTCTGCTGCTGCTGCTGCTGCTGCT	28534	Db	29203	GGTCTCCCTCTAGAGGGGCTCAGTATGAGTTTCTCAAAAGGAGAAAAAATGATATA	29262
Db	28123	CACACATTAACCTTTCTGGAATGCTCTGCTACTCATCTTCTGCTGCTGCTGCTGCTGCT	28182	QY	29608	GTCAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	29667
QY	28535	AACCTTAAAAAACCAGCTCAAGTTCAACCTTCCATTCATTCATTCATTCATTCATTCAT	28594	Db	29263	GTCAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	29322
Db	28183	AACCTTAAAAAACCAGCTCAAGTTCAACCTTCCATTCATTCATTCATTCATTCATTCAT	28242	QY	29668	TCATGAAGAGGGGGAATATAGATATATACATAGAAAAAAGCAATTTCTTGTGTTA	29727
QY	28595	CTTCCCTTAAAGTTTAAAGAACTCAATTTTCAATGATCTTTTGGCATTTTATGACACATGC	28654	Db	29323	TCATGAAGAGGGGGAATATAGATATATACATAGAAAAAAGCAATTTCTTGTGTTA	29382
Db	28243	CTTCCCTTAAAGTTTAAAGAACTCAATTTTCAATGATCTTTTGGCATTTTATGACACATGC	28302	QY	29728	TCAGTAAATACCCAGGGGTAGAAAATGTAAGTAATATATCCCTTCTTCTTCTTCTTCTAG	29787
QY	28655	TTGCTTTGTGTTATTTGTGTTCA-GCCTCATATGCCCAAGGTGTTTATAGACTCCTTAA	28713	Db	29383	TCAGTAAATACCCAGGGGTAGAAAATGTAAGTAATATATCCCTTCTTCTTCTTCTTCTAG	29442
Db	28303	TTGCTTTGTGTTATTTGTGTTCAATGCTCATATGCTTCAATGCTTCAATGCTTCAATGCT	28362	QY	29788	TTCACTTTTGTGACCTTTTATTTTGTGATTTTATGATTTTATGATTTTATGATTTTATG	29847
QY	28714	CGGCAAAATGATGCTTAACACCTTTCTATCTTTTATAGTGTCTTAGTCTGTTGTGT	28773				

Db 29443 TTCACTTTTGGACCTTTATTTTGAAGAAATTCACATGGAAGACATTAACCTCAATTAAGGC 29502
Qy 29848 TTCCAATATTTTGGAGATAAGAAAGGCTGCTATGCTCTTTATAGATGAAACCTTGGGT 29907
Db 29503 TTCCATATTTTGGAGATAAGAAAGGCTGCTATGCTCTTTATAGATGAAACCTTGGGT 29562
Qy 29908 CATTAAATCTAAACAAGACATAAACAAGAAATGGAGCATAAATCTGCAGGTCTCTGAC 29967
Db 29563 CATTAAATCTAAACAAGACATAAACAAGAAATGGAGCATAAATCTGCAGGTCTCTGAC 29622
Qy 29968 TGTAGATTTGGATTTCCAGTTGGTGTCTGTCACCTTTGTTACTCTTCTTAAAGTTATG 30027
Db 29623 TGTAGATTTGGATTTCCAGTTGGTGTCTGTCACCTTTGTTACTCTTCTTAAAGTTATG 29682
Qy 30028 ATCTTTTCTGTGCATPAGGAATTCATAGTATTTCCCATCAACCCCTGGGATTCATAG 30087
Db 29683 ATCTTTTCTGTGCATPAGGAATTCATAGTATTTCCCATCAACCCCTGGGATTCATAG 29742
Qy 30088 CTCTTTTAAGGTCCTCTATGCACTCAATACATCAACAGTAAGTGTCTTTCGAGCACT 30147
Db 29743 CTCTTTTAAGGTCCTCTATGCACTCAATACATCAACAGTAAGTGTCTTTCGAGCACT 29802
Qy 30148 TACTGAGTGATATCATTTGTTGTTCTCACGCAAGCAGCCACAGATCTCACAAAGAACTTAGC 30207
Db 29803 TACTGAGTGATATCATTTGTTGTTCTCACGCAAGCAGCCACAGATCTCACAAAGAACTTAGC 29862
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Db 29863 TGAAGCTGTAGAAATGAATAGTAACTGCTGCAATCCCAATCTGGAGTACTCAAGGGATG 29922
Qy 30268 CAAATGATTCCTTAATTTGACCTTTGCAAGGCTGTGAGTTTGTCTCATGAGAAAGTGGC 30327
Db 29923 CAAATGATTCCTTAATTTGACCTTTGCAAGGCTGTGAGTTTGTCTCATGAGAAAGTGGC 29982
Qy 30328 TACTGATCATGTTATATCTATGTAATGTTGAGCTGCGAAGCATCACTTGAATTTTCC 30387
Db 29983 TACTGATCATGTTATATCTATGTAATGTTGAGCTGCGAAGCATCACTTGAATTTTCC 30042
Qy 30388 AAGCAGAAATACAGCTGATGCAAGCTGCTGAGAAATCGATATTTTCTGAATTC 30447
Db 30043 AAGCAGAAATACAGCTGATGCAAGCTGCTGAGAAATCGATATTTTCTGAATTC 30102
Qy 30448 AGTTCTACGTGGAACAGCTGACTAGTTTCCATTTGCTGTGAAGAAAGGCTCTTTTGTCTTT 30507
Db 30103 AGTTCTACGTGGAACAGCTGACTAGTTTCCATTTGCTGTGAAG-ATGGCTCTTTTGTCTTT 30161
Qy 30508 GGTGATTTTGAATAGGCTTTACTCTGTAGAAAGAGATTTCAATTTGAAGTCCACATC 30567
Db 30162 GGTGATTTTGAATAGGCTTTACTCTGTAGAAAGAGATTTCAATTTGAAGTCCACATC 30221
Qy 30568 AGGATTTGGTTCAACAACTGGAGTACAGGTTTTCAGAAATATCTCTTTAATCTCCAA 30627
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Qy 30628 TAATAAATTTTCTCATCTAATTTCTGAGAACTTCACTTCTGAGCGGAGCATATAG 30687
Db 30282 TAATAAATTTTCTCATCTAATTTCTGAGAACTTCACTTCTGAGCGGAGCATATAG 30341
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Db 30342 ATAGATTTTGTCTCACTGTTTCTGATTTGCCACTTTCACCTTTCCTTTTCAACTAGGTT 30401
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RESULT 8
 AL391648/c

LOCUS AL391648 Homo sapiens chromosome 10 clone RP11-203A7, 9 unordered pieces.
 DEFINITION Homo sapiens chromosome 10 clone RP11-203A7, 9 unordered pieces.
 ACCESSION AL391648

VERSION AL391648.12 GI:14669309

KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Chapman,J.

Direct Submission

Submitted (17-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

On Jul 10, 2001 this sequence version replaced gi:14596357.

COMMENT

----- Genome Center

Center: Sanger Centre

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: BA203A7

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 174005 bases at least Q40

Consensus quality: 174806 bases at least Q30

Consensus quality: 175273 bases at least Q20

Insert size: 175632; sum-of-contigs

Insert size: 155595; 14.1% error; agarose-fp

Quality coverage: 6.85x in Q20 bases; sum-of-contigs Quality

coverage: 8.13x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently

* consists of 9 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.

* as soon as it is available and the accession number will

* be preserved.

* 1 23099: contig of 23099 bp in length

* * 23100 23199: gap of 100 bp


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* 23200 38049: contig of 14850 bp in length
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 2279 AATTAAATCACTAGCTGATTAAGCCCAACAGAGAGTCAAGCTTTTGTGAAGCTT 2338
 42681 AATTAAATCACTAGCTGATTAAGCCCAACAGAGAGTCAAGCTTTTGTGAAGCTT 42622
 2339 TGAAGCCAGGCTGCTCTCTCTGTTACAAAAGTCTTAAATGCACTTCTTCTCC 2398
 42621 TGAAGCCAGGCTGCTCTCTCTGTTACAAAAGTCTTAAATGCACTTCTTCTCC 42562
 2399 AATATAAGGCTGTTTATCTACATTTGAAATCTGTTTGTAGTGAAGCTTCAATCA 2458
 42561 AATATAAGGCTGTTTATCTACATTTGAAATCTGTTTGTAGTGAAGCTTCAATCA 42502
 2459 TGATACTATCTAGATCTCTTGGATTAATCTTGTGAGCTTCTACATCAGCATTTGCTACTC 2518

42501 TGATACTATCTAGATCTCTTGGATAAATTTGTGAGCTTCTACATCAGCATTTGCTACTTC 42442
 2519 ACCTTGTACTCTTATGTAATGGAGTGGCATCTTTCTCGTACCTCATGAACCAACCTCTG 2578
 42441 ACCTTGTACTCTTATGTAATGGAGTGGCATCTTTCTCGTACCTCATGAACCAACCTCTG 42382
 2579 CTAGCTTCCAACTTTTCTTCTGTAGTTTCTCGCTCTCTCAGCCTTCATAGACTTGAGG 2638
 42381 CTAGCTTCCAACTTTTCTTCTGTAGTTTCTCGCTCTCTCAGCCTTCATAGACTTGAGG 42322
 2639 ATAGTTAGAGACTTGTCTTGGATTAGATTTTGGCTTCAGGAATGTTGGCTGGTTTGA 2698
 42321 ATAGTTAGAGACTTGTCTTGGATTAGATTTTGGCTTCAGGAATGTTGGCTGGTTTGA 42262
 2699 TCTTCTATCCAGACCACTAAACCTTTATCCATATCAGCAATTAAGGCTGTTTGTCTTCTT 2758
 42261 TCTTCTATCCAGACCACTAAACCTTTATCCATATCAGCAATTAAGGCTGTTTGTCTTCTT 42202
 2759 ATTATTTGTGTCTTCTGAGTAGACATTTTAAATTTGCTTCAAGATATATTTCTTGA 2818
 42201 ATTATTTGTGTCTTCTGAGTAGACATTTTAAATTTGCTTCAAGATATATTTCTTGA 42142
 2819 TTCAACACTTTGGCTGACTGTCAGAGGCTAGCTTTTCAAGATATATTTCTTGA 2878
 42141 TTCAACACTTTGGCTGACTGTCAGAGGCTAGCTTTTCAAGATATATTTCTTGA 42082
 2879 TGCCTTCTCACTAAGCTTAAATCATTTCTAGCTTTTGAATTTAAATAGAGATGTTAGGCT 2938
 42081 TGCCTTCTCACTAAGCTTAAATCATTTCTAGCTTTTGAATTTAAATAGAGATGTTAGGCT 42022
 2939 AGGCACAGTGCAGGACAGTGGCATATGCTGTAATTTCAACACATTAAGAGGCCAAG 2998
 42021 AGGCACAGTGCAGGACAGTGGCATATGCTGTAATTTCAACACATTAAGAGGCCAAG 41962
 2999 TGGAGGATTTGCTTGAACCCAGGAGTGGAGTTGTAGAGATCACACCATGCTGCTTCCGT 3058
 41961 TGGAGGATTTGCTTGAACCCAGGAGTGGAGTTGTAGAGATCACACCATGCTGCTTCCGT 41902
 3059 CCTGGATGACAGAGCAAGA-CTTTTCTCAAAATTAATAGAGGCTGCTTCTTCTTTT 3117
 41901 CCTGGATGACAGAGCAAGACCTTTTCTCAAAATTAATAGAGGCTGCTTCTTCTTTT 41842
 3118 GTTTGAGCCCATAGAGCCCATAGTATGATTTTAAATTTGGCTTAAATCAATCTGTTGTG 3177
 41841 GTTTGAGCCCATAGAGCCCATAGTATGATTTTAAATTTGGCTTAAATCAATCTGTTGTG 41782
 3178 TCTCAGAGATAGGAGGCTCTGAAGAGGAGAGAGTGGGGGAATGCTGCTGAGTGG 3237
 41781 TCTCAGAGATAGGAGGCTCTGAAGAGGAGAGAGTGGGGGAATGCTGCTGAGTGG 41722
 3238 AGCAGTCAGAGCAACACATTAACATTAATTTGCTGCTTATATGATGCTGTTG 3297
 41721 AGCAGTCAGAGCAACACATTAACATTAATTTGCTGCTTATATGATGCTGTTG 41662
 3298 TGATGCCCCCAACAAATTAACATTAAGTTACAGCAATATCACTGATCACAGATCACCATAA 3357
 41661 TGATGCCCCCAACAAATTAACATTAAGTTACAGCAATATCACTGATCACAGATCACCATAA 41602
 3358 CAGATTAAGATCATCGCAAGTTTGAATATTTCTTGAATTTAGCAAGTGTGACACA 3417
 41601 CAGATTAAGATCATCGCAAGTTTGAATATTTCTTGAATTTAGCAAGTGTGACACA 41543
 3418 GAGAAACAAAGTAGACACATGCTGCTTGAATAATTTGCTGCTTATGATGCTGCTCATCG 3477
 41542 GAGAAACAAAGTAGACACATGCTGCTTGAATAATTTGCTGCTTATGATGCTGCTCATCG 41484
 3478 CAAGTTTCCCATAGCCCTTCAATTTAATAAACAACATATCTAGGAAGTTCATTAAGT 3537
 41483 TAAGTTTCCCATAGCCCTTCAATTTAATAAACAACATATCTAGGAAGTTCATTAAGT 41424
 3538 GAAGTGAATAAGTAGAGTATGCTGTAATATTTTCAAGCTTTCAGAGCATAGGCTT 3597

Dd	41423	GAAGTGAATGAAGTATGCTGTGTAATATTTACAGCTTTCCAGACCATAGGGTTT	41364
Qy	3598	CTGTGCAACTGCTCACCCTCGCAATATATAGCATGAAGCAGCATATAGAAAATATACATA	3657
Dd	41363	CTGTGCAACTGCTCACCCTCGCAATATATAGCATGAAGCAGCATATAGAAAATATACATA	41304
Qy	3658	AATGAGCCCTGTAATCCCAACACTTTGGGAGCCCAAGGTGGATCGATCACTTGAGGTGAC	3717
Dd	41303	AATGAGCCCTGTAATCCCAACACTTTGGGAGCCCAAGGTGGATCGATCACTTGAGGTGAC	41244
Qy	3718	GAATTCGAGACCAAGCTTGGCCCAACATGGGCAAAACCCCGCTCTCTACTAAAATAACAAAAT	3777
Dd	41243	GAATTCGAGACCAAGCTTGGCCCAACATGGGCAAAACCCCGCTCTCTACTAAAATAACAAAAT	41184
Qy	3778	GAGCAGGACTACGATGCGCTGATGCCAGCTACTTTGGAGGCTGAGCAGAGAACTCT	3837
Dd	41183	GAGCAGGACTACGATGCGCTGATGCCAGCTACTTTGGAGGCTGAGCAGAGAACTCT	41124
Qy	3838	CTTGAACCCGGGAGGGAGGTTACAGTGAGCCAAAGATTGTGCACCTGCACCTCCAGCCTG	3897
Dd	41123	CTTGAACCCGGGAGGGAGGTTACAGTGAGCCAAAGATTGTGCACCTGCACCTCCAGCCTG	41064
Qy	3898	GGCAACAGAGTGAGACTGTCTCAAAATAAATAAAGGAAAGAAAATACACATAAATG	3957
Dd	41063	GGCAACAGAGTGAGACTGTCTCAAAATAAATAAAGGAAAGAAAATACACATAAATG	41004
Qy	3958	AATGTATGTGCTGTACAGTATATCTCATGCTCTAGCTTGCCAAACCCCTGCTTAC	4017
Dd	41003	AATGTATGTGCTGTACAGTATATCTCATGCTCTAGCTTGCCAAACCCCTGCTTAC	40944
Qy	4018	ACTGTCAGTTACCTTCTAAGAGATTAAAAATCATAAACATATCTATTACGTTTATTCAC	4077
Dd	40943	ACTGTCAGTTACCTTCTAAGAGATTAAAAATCATAAACATATCTATTACGTTTATTCAC	40884
Qy	4078	ATCCTAGTGATCTTCTCTCTATAGTAAATCAAAATTCATTCCTGGTATCATATTTCTTC	4137
Dd	40883	ATCCTAGTGATCTTCTCTCTATAGTAAATCAAAATTCATTCCTGGTATCATATTTCTTC	40824
Qy	4138	TTTCTAAATTAATTCCTTTAAATTTTATAGCACAGTCTAAATAGCAATGCATATGCG	4197
Dd	40823	TTTCTAAATTAATTCCTTTAAATTTTATAGCACAGTCTAAATAGCAATGCATATGCG	40764
Qy	4198	AATCATGCTATAGACCTGCTATAAAATAGCAATGAATTAATGATGATGATTTATTTG	4257
Dd	40763	AATCATGCTATAGACCTGCTATAAAATAGCAATGAATTAATGATGATGATTTATTTG	40704
Qy	4258	TCGGAATAAGTTTCTTTGAAATATACCTTCTGGGTATATAAATCCATGTTCA	4317
Dd	40703	TCGGAATAAGTTTCTTTGAAATATACCTTCTGGGTATATAAATCCATGTTCA	40644
Qy	4318	TAACTTCTCTTTCTTTCAGACCTTAAATGAAGTCACTCAGTTATCTTCTGGCTGTATAG	4377
Dd	40643	TAACTTCTCTTTCTTTCAGACCTTAAATGAAGTCACTCAGTTATCTTCTGGCTGTATAG	40584
Qy	4378	TTTCTCTGGCTGCTTCAAGATTTTCTATGCTTTTAAATTTTAGCAGTTTATGATGTC	4437
Dd	40583	TTTCTCTGGCTGCTTCAAGATTTTCTATGCTTTTAAATTTTAGCAGTTTATGATGTC	40524
Qy	4438	TAGAGTGATTTCTTTGATTTATCTTTTGGGGCCCTTAAATTTCTTTCATCTTTT	4497
Dd	40523	TAGAGTGATTTCTTTGATTTATCTTTTGGGGCCCTTAAATTTCTTTCATCTTTT	40464
Qy	4498	TTTCTTTTCTTTTCTTTTAAATTCAGTTTGTGCTGCTCCCTCAAGTGGGCTGAAAAAA	4557
Dd	40463	TTTCTTTTCTTTTCTTTTAAATTCAGTTTGTGCTGCTCCCTCAAGTGGGCTGAAAAAA	40404
Qy	4558	AGCAAAAATAAATCATAGTTTAAATAAATTAATTTGGAATAATTTTACGATCATCTTCT	4617
Dd	40403	AGCAAAAATAAATCATAGTTTAAATAAATTAATTTGGAATAATTTTACGATCATCTTCT	40344
Qy	4618	TCAATATTTATCTACTATGCTCCCTCTCTCCCTTCTCTGCTGCTGCTGCTGCTGCTGCT	4677
Dd	40343	TCAATATTTATCTACTATGCTCCCTCTCTCCCTTCTCTGCTGCTGCTGCTGCTGCTGCT	40284

Db	37109	GGAGCCCTCGTGGTCAGGATAGAGAGAAAGACCTTGGAGTTGAGCCCTTGAACAGTATTTA	37050
Qy	7974	ATATTCAAAGGTTAAGAGAGAGAGCAATTTAGAGGGGAGAAATAGTTCAGACCAAAAT	8033
Db	37049	ATATTCAAAGGTTAAGAGAGAGAGCAATTTAGAGGGGAGAAATAGTTCAGACCAAAAT	36990
Qy	8034	GATGGTGTCAAGATGAACACAGTCAGTAAAGAGCAGACTGGTCTGGATGGAGAGGAGA	8093
Db	36989	GATGGTGTCAAGATGAACACAGTCAGTAAAGAGCAGACTGGTCTGGATGGAGAGGAGA	36930
Qy	8094	TTTGCAATCTTGGGATTAAGTCAATTTAGACCTTGAAGCCAGGATTAAGTAAAGCCAC	8153
Db	36929	TTTGCAATCTTGGGATTAAGTCAATTTAGACCTTGAAGCCAGGATTAAGTAAAGCCAC	36870
Qy	8154	AGTGAAGCGACTGCTCGTATGAAGCTTATTTAAGAGATTAATCTGGTAGTGACAT	8213
Db	36869	AGTGAAGCGACTGCTCGTATGAAGCTTATTTAAGAGATTAATCTGGTAGTGACAT	36810
Qy	8214	GTGCCAAAACTGAATAGGTAGAAATGAGATGAGAGAGCCAGTGTAGAACTAAGTCTGG	8273
Db	36809	GTGCCAAAACTGAATAGGTAGAAATGAGATGAGAGAGCCAGTGTAGAACTAAGTCTGG	36750
Qy	8274	TGCAGTAATCGAGATTGAGCAATAAACACCAAACTACAGTATCACAGATAAATGGATG	8333
Db	36749	TGCAGTAATCGAGATTGAGCAATAAACACCAAACTACAGTATCACAGATAAATGGATG	36690
Qy	8334	TTTGAACGGACGGTTTAAAGGAAAAATTTGATGGTATTTGGTAAATTTATTAGATAATCCAGG	8393
Db	36689	TTTGAACGGACGGTTTAAAGGAAAAATTTGATGGTATTTGGTAAATTTATTAGATAATCCAGG	36630
Qy	8394	GCCATGGAATGAGAGGGGAAAAATGACATAACATAGTCATCAAAATGGTTTTCTTAAATGAA	8453
Db	36629	GCCATGGAATGAGAGGGGAAAAATGACATAACATAGTCATCAAAATGGTTTTCTTAAATGAA	36570
Qy	8454	TCTGAATTTTGGTGTGAAGCAACATTTTCTTAGGCTTGCCTAGTTGGTACAGCTGACT	8513
Db	36569	TCTGAATTTTGGTGTGAAGCAACATTTTCTTAGGCTTGCCTAGTTGGTACAGCTGACT	36510
Qy	8514	ATGATAATGACTGCTACCATGCTTGTTCCTTTTATAGCAGCTGTGATCCCCACACAGCC	8573
Db	36509	ATGATAATGACTGCTACCATGCTTGTTCCTTTTATAGCAGCTGTGATCCCCACACAGCC	36450
Qy	8574	AAACATAGCCCTCTGAAAGAGCAGATGCTTTTCACTCTCTCCAAAGTGTGGCAAA	8633
Db	36449	AAACATAGCCCTCTGAAAGAGCAGATGCTTTTCACTCTCTCCAAAGTGTGGCAAA	36390
Qy	8634	TAGAGAGCCCTTTGAAGTACTTTATAGTTAGGGGTTCCAGTGAGTATTTGAAATATTA	8693
Db	36389	TAGAGAGCCCTTTGAAGTACTTTATAGTTAGGGGTTCCAGTGAGTATTTGAAATATTA	36330
Qy	8694	AGTCATGCCGTGGTTGACAGCATGGCCCTACTGCTCATCATCAGCTATTAACCTTAGGC	8753
Db	36329	AGTCATGCCGTGGTTGACAGCATGGCCCTACTGCTCATCATCAGCTATTAACCTTAGGC	36270
Qy	8754	AAGTTAATGAACCTTTCTAAGCCCGAGTCTACTCATTTATAAAGTGGGATTTAATAAT	8813
Db	36269	AAGTTAATGAACCTTTCTAAGCCCGAGTCTACTCATTTATAAAGTGGGATTTAATAAT	36210
Qy	8814	GTCTACTTCATAAAATPATGAACCTGAGTTAGGTCAATTCAGATAGTGTAGTCTGATT	8873
Db	36209	GTCTACTTCATAAAATPATGAACCTGAGTTAGGTCAATTCAGATAGTGTAGTCTGATT	36150
Qy	8874	CTTCGRACCTAGTAAACAGTCAGTAAACAGCAAAATGCCACATGCCGTGATTATATCC	8933
Db	36149	CTTCGAACCTTAGTAAACAGTCAGTAAACAGCAAAATGCCACATGCCGTGATTATATCC	36090
Qy	8934	AAGGGGAGAAAGGTAAAAGTGAATTTTCATGATTTTAGGATTCAAATATATCATTTCAA	8993
Db	36089	AAGGGGAGAAAGGTAAAAGTGAATTTTCATGATTTTAGGATTCAAATATATCATTTCAA	36030
Qy	8994	AGATGCTTTATAGCTATGCTTTTGGTAAAGAAATGAGCTGAAACAGAAATTTTCTGAC	9053
Db	36029	AGATGCTTTTATAGCTATGCTTTTGGTAAAGAAATGAGCTGAAACAGAAATTTTCTGAC	35970
Qy	9054	AGCAGTGATTATTAATAGGTGAAAATAGGCTATTGATGTCCTTTAGAGGATATAGATGTCA	9113
Db	35969	AGCAGTGATTATTAATAGGTGAAAATAGGCTATTGATGTCCTTTAGAGGATATAGATGTCA	35910
Qy	9114	CCTTTTGCATATAAGTGCACAAAATTCACATAAGTATGTCGTCTACACAGAGAGA	9173
Db	35909	CCTTTTGCATATAAGTGCACAAAATTCACATAAGTATGTCGTCTACACAGAGAGA	35850
Qy	9174	GAGACGTGAGAGCAATTAAGTTAGTAAACATCCCTCGCTCGCTTTTTTTTTTTTGGACAG	9233
Db	35849	GAGACGTGAGAGCAATTAAGTTAGTAAACATCCCTCGCTCGCTTTTTTTTTTTTGGACAG	35790
Qy	9234	GGTCTTACTCTGTTGGCTGAGTGCAGTGGTGAATCAATCGTGGCTCACTGAGTCTC	9293
Db	35789	GGTCTTACTCTGTTGGCTGAGTGCAGTGGTGAATCAATCGTGGCTCACTGAGTCTC	35730
Qy	9294	AACATCTCGGCTCAAGCGATCTCTCGCTCAGCTCTCTGAGTAGTGCAGTGTGCACCA	9353
Db	35729	AACATCTCGGCTCAAGCGATCTCTCGCTCAGCTCTCTGAGTAGTGCAGTGTGCACCA	35670
Qy	9354	CCACACCCGGCTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	9413
Db	35659	CCACACCCGGCTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	35610
Qy	9414	AGGTCTCAAACTCTGAGCTCAAGCAATCTGCTCACTTCAGCTCCAAAAATGCTGGAT	9473
Db	35609	AGGTCTCAAACTCTGAGCTCAAGCAATCTGCTCACTTCAGCTCCAAAAATGCTGGAT	35550
Qy	9474	TACAGGCTGAGCACACAGCTGGCCAGTAAACCCCATTCATTTACATCATCTTACTTG	9533
Db	35549	TACAGGCTGAGCACACAGCTGGCCAGTAAACCCCATTCATTTACATCATCTTACTTG	35490
Qy	9534	TCCCTCCAAAACTCTGCAAGTAGGTAGTCTCTCTTTTATTTAGGTGAAGAA	9593
Db	35489	TCCCTCCAAAACTCTGCAAGTAGGTAGTCTCTCTTTTATTTAGGTGAAGAA	35430
Qy	9594	CTTGAAGTGGTGTGAGGAATAGTGTTTTCCCAAGAGTCAAGCAGCTGGAGTGGCAGAG	9653
Db	35429	CTTGAAGTGGTGTGAGGAATAGTGTTTTCCCAAGAGTCAAGCAGCTGGAGTGGCAGAG	35370
Qy	9654	CTGTATATCTCTTCTGATTTCCACCAAGCTGTTTATCATCACATCTGGAGAAAGTCTCTG	9713
Db	35369	CTGTATATCTCTTCTGATTTCCACCAAGCTGTTTATCATCACATCTGGAGAAAGTCTCTG	35310
Qy	9714	AGGCACAGATGTTTAGTGGGAGGATGAGACACAGGCTGCAATGCTTAAAGATAATCGG	9773
Db	35309	AGGCACAGATGTTTAGTGGGAGGATGAGACACAGGCTGCAATGCTTAAAGATAATCGG	35250
Qy	9774	AATAAAGCAGAAACAAAGCGTTTCTGTTTAAATGAGACAGAAATAAGCGGTTT	9833
Db	35249	AATAAAGCAGAAACAAAGCGTTTCTGTTTAAATGAGACAGAAATAAGCGGTTT	35190
Qy	9834	GTTGTTTGGGATTTGAGCACTTGGAGAGTGGGAGCGATTTGATTTGGGTGAGACTGCTC	9893
Db	35189	GTTGTTTGGGATTTGAGCACTTGGAGAGTGGGAGCGATTTGATTTGGGTGAGACTGCTC	35130
Qy	9894	CTGGAATCTCGATCTGTTCTGGACACTCATTTACTAGGCTTATAGAACTAGCTGGAG	9953
Db	35129	CTGGAATCTCGATCTGTTCTGGACACTCATTTACTAGGCTTATAGAACTAGCTGGAG	35070
Qy	9954	GAGGTTCAAAAGAAAGCTCCAAAATGATTAGCGGCTGACGGGATTTGATTTATAGAAAT	10013
Db	35069	GAGGTTCAAAAGAAAGCTCCAAAATGATTAGCGGCTGACGGGATTTGATTTATAGAAAT	35010
Qy	10014	ATTAAGAAATTAATGTTATAGCTAGCTAAAGCAAGATGAAGAGACAGCTTAAATG	10073
Db	35009	ATTAAGAAATTAATGTTATAGCTAGCTAAAGCAAGATGAAGAGACAGCTTAAATG	34950
Qy	10074	TATACAAATATCTGAAACGTCGCAACCTTTAAAGAGAGGATTAATTTTAAACATGATAC	10133
Db	34949	TATACAAATATCTGAAACGTCGCAACCTTTAAAGAGAGGATTAATTTTAAACATGATAC	34890

Qy	10134	ACGGGGCACAATATGAGTACAGGATGAAATTTTTCAGTGTATCTAGAGAAATTC	10193	Db	33809	TGTAGACATGAGTGGAGCTCTAAGTGTCTTCAATAGCAAAACACTAGTTTTT	33750
Db	34889	ACGGGGCACAATATGAGTACAGGATGAAATTTTTCAGTGTATCTAGAGAAATTC	34830	Qy	11274	CTTTCTTTTTTTTTTTTTTTGGAGACAGAGTCTTGTCTGTGCGCCAGGCTGGAGTCA	11333
Qy	10194	CCGATAGTGAATCTGTTAAGGCTCTCTGTAGTGTGGCTTTCCCTCGAGAGGCAATAGAA	10253	Db	33749	CTTTCTTTTTTTTTTTTTTTGGAGACAGAGTCTTGTCTGTGCGCCAGGCTGGAGTCA	33690
Db	34829	CCGATAGTGAATCTGTTAAGGCTCTCTGTAGTGTGGCTTTCCCTCGAGAGGCAATAGAA	34770	Qy	11334	ATGCGACGATCTCGCTCACTGAACTCTGCTCCCGGTTCAAGCGACTCTCTGCTCA	11393
Qy	10254	ATTTCAGTCTTACGATTTTAAAGTTTCTTGGAACTAGTATTAGATGATGTAGAGA	10313	Db	33689	ATGCGACGATCTCGCTCACTGAACTCTGCTCCCGGTTCAAGCGACTCTCTGCTCA	33630
Db	34769	ATTTCAGTCTTACGATTTTAAAGTTTCTTGGAACTAGTATTAGATGATGTAGAGA	34710	Qy	11394	GCCTCCCGAGTGTGGGATTTACAGTGTGCGCCACACCCAGCCAGCTTAATTTTCTATTT	11453
Qy	10314	ATTATTATTAATTTGGTCAAGTATGATTAATGTTGTTAGTCTTAAGAAATTTGAT	10373	Db	33629	GCCTCCCGAGTGTGGGATTTACAGTGTGCGCCACACCCAGCCAGCTTAATTTTCTATTT	33570
Db	34709	ATTATTATTAATTTGGTCAAGTATGATTAATGTTGTTAGTCTTAAGAAATTTGAT	34650	Qy	11454	TTAGTAGAGATGAGTTTCAACGTTTGGCCAGGCTGCTCAAACTCTGCGCTCAAGT	11513
Qy	10374	TTTTTAGAGTACATACCTGAAATATAGCATAGAAATGATGTAGGAGATTTGCTTTA	10433	Db	33569	TTAGTAGAGATGAGTTTCAACGTTTGGCCAGGCTGCTCAAACTCTGCGCTCAAGT	33510
Db	34649	TTTTTAGAGTACATACCTGAAATATAGCATAGAAATGATGTAGGAGATTTGCTTTA	34590	Qy	11514	GATCCGCTGCTTGGCTCCCAAGTCTCGGATTTACAGTGTGAGCCACACACCCAG	11573
Qy	10434	AAATACACAGTAAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10493	Db	33509	GATCCGCTGCTTGGCTCCCAAGTCTCGGATTTACAGTGTGAGCCACACACCCAG	33450
Db	34589	AAATACACAGTAAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	34530	Qy	11574	CTGCAAAACCCCTATTTTTCTTGAATGGAGAAACACTTTTCCCTTTATTTAGTGTGG	11633
Qy	10494	AAAAAGGCAAGAGAGAGAGGTAAGAGAAAGAAAGAAATGAAGGAGAGGCT	10553	Db	33449	CTGCAAAACCCCTATTTTTCTTGAATGGAGAAACACTTTTCCCTTTATTTAGTGTGG	33390
Db	34529	AAAAAGGCAAGAGAGAGAGGTAAGAGAAAGAAAGAAATGAAGGAGAGGCT	34470	Qy	11634	AAGCAAGAGAGGAGGTAATTCATTAAGTGAATAATTTCCAAATCCAGAAACATCGATA	11693
Qy	10554	GGGCACTGTGGCTCATGCTTAATCCAGCATTTAGGAGGCCAGTGTGGAGGATCACT	10613	Db	33389	AAGCAAGAGAGGAGGTAATTCATTAAGTGAATAATTTCCAAATCCAGAAACATCGATA	33330
Db	34469	GGGCACTGTGGCTCATGCTTAATCCAGCATTTAGGAGGCCAGTGTGGAGGATCACT	34410	Qy	11694	AGCAGCAGCTTAATTTTTTAAAGAGAAATTTTTTAACTATCTTTTGAAGCTCTTT	11753
Qy	10614	TAATTAAGCCAGGAGTTCAAGCTGCAGTGTGATTTGGCCACTGCACTCCAGCC	10673	Db	33329	AGCAGCAGCTTAATTTTTTAAAGAGAAATTTTTTAACTATCTTTTGAAGCTCTTT	33270
Db	34409	TAATTAAGCCAGGAGTTCAAGCTGCAGTGTGATTTGGCCACTGCACTCCAGCC	34350	Qy	11754	AGGAGACCTCACTGCTTCCCTTGATTTGAGGTGGAATCCAGGA-CTTTTGA	11812
Qy	10674	TGGGTGCAGAGTGAAGCCCTGTCTTAAAAAATAATAGTTAAAAAGAAAGAAAG	10733	Db	33269	AGGAGACCTCACTGCTTCCCTTGATTTGAGGTGGAATCCAGGAGGTTTGA	33210
Db	34349	TGGGTGCAGAGTGAAGCCCTGTCTTAAAAAATAATAGTTAAAAAGAAAGAAAG	34290	Qy	11813	ATGATAGCTTATGCTGCTTTTTTGTGTTAGAGAAATATAAATATTTATCTAGGTT	11872
Qy	10734	GATAGATGAAGTGAAGAGTGTGTAATGTTGAACCTGAAGGAGTAAATATGTGAG	10793	Db	33209	ATGATAGCTTATGCTGCTTTTTTGTGTTAGAGAAATATAAATATTTATCTAGGTT	33150
Db	34289	GATAGATGAAGTGAAGAGTGTGTAATGTTGAACCTGAAGGAGTAAATATGTGAG	34230	Qy	11873	TTGCTGATGAGTGAAGTGAAGCAACACCCACTGTTTGAAGAGTGAATTTCTGAAT	11932
Qy	10794	TTCACTTCTCTTCAAGTCTTTTATGATGTTTCCCACTTTTCAATAAACAATTTA	10853	Db	33149	TTGCTGATGAGTGAAGTGAAGCAACACCCACTGTTTGAAGAGTGAATTTCTGAAT	33090
Db	34229	TTCACTTCTCTTCAAGTCTTTTATGATGTTTCCCACTTTTCAATAAACAATTTA	34170	Qy	11933	TTCTGACAGTGCACATCTAGGCGAGCAATGGCAGTGAAGTGAAGTGAATTTAGCTCA	11992
Qy	10854	AATTAATTTTCTGATCAAACTTAGTACAGTATTAATCCCTGGCTTCCCTGACTAGA	10913	Db	33089	TTCTGACAGTGCACATCTAGGCGAGCAATGGCAGTGAAGTGAAGTGAATTTAGCTCA	33030
Db	34169	AATTAATTTTCTGATCAAACTTAGTACAGTATTAATCCCTGGCTTCCCTGACTAGA	34110	Qy	11993	GTGTAAGATGAATCCAGAAACCATCGGCTCTGACTGAAGTGAAGCGGCGGCTTG	12052
Qy	10914	ACAGCCTCATTAACACATGGGAGAGTTCTGGCCGACAGGACACGAGTGGTTTCAAC	10973	Db	33029	GTGTAAGATGAATCCAGAAACCATCGGCTCTGACTGAAGTGAAGCGGCGGCTTG	32970
Db	34109	ACAGCCTCATTAACACATGGGAGAGTTCTGGCCGACAGGACACGAGTGGTTTCAAC	34050	Qy	12053	TGGGAAAGCTGGCTGGAGTCTCTCTATAAGCAGGCAATCTTTTCTCCAGCCGCTCACT	12112
Qy	10974	ATCTTGTCTGTTAATGTGTCTGGAGTGAAGGCCCTTTCTAAGTGTGATAGATAAT	11033	Db	32969	TGGGAAAGCTGGCTGGAGTCTCTCTATAAGCAGGCAATCTTTTCTCCAGCCGCTCACT	32910
Db	34049	ATCTTGTCTGTTAATGTGTCTGGAGTGAAGGCCCTTTCTAAGTGTGATAGATAAT	33990	Qy	12113	GTGTTGTTGGGCCACGGTAAAGCTCTGCGCTCTAGGCTGTAAACCCCAACATCTCTC	12172
Qy	11034	CCAGGAAACTTGTATGAACCTGCAGACCTATCAGGCTACCTGAGGAGGTGAGTCTACTAA	11093	Db	32909	GTGTTGTTGGGCCACGGTAAAGCTCTGCGCTCTAGGCTGTAAACCCCAACATCTCTC	32850
Db	33989	CCAGGAAACTTGTATGAACCTGCAGACCTATCAGGCTACCTGAGGAGGTGAGTCTACTAA	33930	Qy	12173	CTCTGCTCCCTCCAGAGTGTGTTCTGAAGCAAACTGGATGTCTATTCCTCCCTCTCTG	12232
Qy	11094	GGTGAAGACAGAGGCGAGGTCTGTATAGCAGTGAACCCGCTCTCTTTTCTGTCT	11153	Db	32849	CTCTGCTCCCTCCAGAGTGTGTTCTGAAGCAAACTGGATGTCTATTCCTCCCTCTCTG	32790
Db	33929	GGTGAAGACAGAGGCGAGGTCTGTATAGCAGTGAACCCGCTCTCTTTTCTGTCT	33870	Qy	12233	AACCTCTAGCACCTTACAGGAGCTCCCTCTGCTGCGCCACATACCTTCAACAGTAGACAT	12292
Qy	11154	CCTCATTCGTGGAATTTAGTGGAGTCTCAATTTTGAAGTGGAGCTCTAAGTAGTCCACT	11213	Db	32789	AACCTCTAGCACCTTACAGGAGCTCCCTCTGCTGCGCCACATACCTTCAACAGTAGACAT	32730
Db	33869	CCTCATTCGTGGAATTTAGTGGAGTCTCAATTTTGAAGTGGAGCTCTAAGTAGTCCACT	33810	Qy	12293	TCCTAATGAAGATTTGATTAATTTGTAATTAAGTGTCTTCAAGTGTCTTCTAGTTGGC	12352
Qy	11214	TGTAGACATGAGTGGAGCTCTAAGTGTCTTCAAGTGTCTTCAAGTGTCTTCTAGTTGGC	11273				

Db	28379	ATGATCTCAGATTTCATCAGTGTGGCTGATGTTTAAACCCAGGGACAGGATAAGAGG	28320
QY	16710	TTATTCAGGAGAGCGGTAGATAAGAAAGCTTAATGGCTTCTGGCTCTTAGTCATTCAA	16769
Db	28319	TTATTCAGGAGAGCGGTAGATAAGAAAGCTTAATGGCTTCTGGCTCTTAGTCATTCAA	28260
QY	16770	AATCGGACCTCTGAGGACGAGGAAAGCCAGAAAGAGTAGATTTCCTGGGACTCACGGGA	16829
Db	28259	AATCGGACCTCTGAGGACGAGGAAAGCCAGAAAGAGTAGATTTCCTGGGACTCACGGGA	28200
QY	16830	TAAAGACTTTCAAAGTGGGGTGGCGTGCAGTGTCTGTAAGAAAGTAGAGTTCCTGGGACTCACGGGA	16889
Db	28199	TAAAGACTTTCAAAGTGGGGTGGCGTGCAGTGTCTGTAAGAAAGTAGAGTTCCTGGGACTCACGGGA	28140
QY	16890	CAGAAGGATTAATCGTTGGACCTCGAGAACTTGAATTTTAAAGTTGGTAAAGCTTTA	16949
Db	28139	CAGNAGGATTAATCGTTGGACCTCGAGAACTTGAATTTTAAAGTTGGTAAAGCTTTA	28080
QY	16950	AAAAAGAGCAATTTAGATACCTTTTGAATTTTGAAGATTTGTTGGTATATGTGT	17009
Db	28079	AAAAAGAGCAATTTAGATACCTTTTGAATTTTGAAGATTTGTTGGTATATGTGT	28020
QY	17010	TATTCAGGACAAAGGACAGAAAGTAAATAATCTTACTGAAAGTTCAGTATGCTT	17069
Db	28019	TATTCAGGACAAAGGACAGAAAGTAAATAATCTTACTGAAAGTTCAGTATGCTT	27960
QY	17070	GGCACTGTAAACACCCCTGTTTAAATTTCTACGGCAACCTATAGAGTAGGTGTCAATCCC	17129
Db	27959	GGCACTGTAAACACCCCTGTTTAAATTTCTACGGCAACCTATAGAGTAGGTGTCAATCCC	27900
QY	17130	CATCTTACAGATGAGGATGAGGTGAGCTAGATTAAAGAGTTTCCCTCAGGTTACAC	17189
Db	27899	CATCTTACAGATGAGGATGAGGTGAGCTAGATTAAAGAGTTTCCCTCAGGTTACAC	27840
QY	17190	AACTGGTTAACGTAGAGTAGGATTTGAACCCGGATGGGTGATCCAGAGCTCATGCTT	17249
Db	27839	AACTGGTTAACGTAGAGTAGGATTTGAACCCGGATGGGTGATCCAGAGCTCATGCTT	27780
QY	17250	TAAATCGCTAGACTGTGCTCAAGAAAGCTGGACCGCAAAAAAATTAATAAAAAATA	17309
Db	27779	TAAATCGCTAGACTGTGCTCAAGAAAGCTGGACCGCAAAAAAATTAATAAAAAATA	27720
QY	17310	AGGAGCCCTGGCTAGCAAAATAGGAGTTGTTCAGACAGATGTGAAGAAAGCAAG	17369
Db	27719	AGGAGCCCTGGCTAGCAAAATAGGAGTTGTTCAGACAGATGTGAAGAAAGCAAG	27660
QY	17370	GCAGAGGAAAGTCACTGTACAGAGAGAGACCCATCAGCAGAGACAGTGAGCTGG	17429
Db	27659	GCAGAGGAAAGTCACTGTACAGAGAGAGACCCATCAGCAGAGACAGTGAGCTGG	27600
QY	17430	TAAAGTGGCTGGCGATCAGCCCTGAAATACCTCCAGAGAGGCGGCTCAGGCTGTA	17489
Db	27599	TAAAGTGGCTGGCGATCAGCCCTGAAATACCTCCAGAGAGGCGGCTCAGGCTGTA	27540
QY	17490	ATCCAGCACTTTGGGAGGCGAGGTGGCGAGATCACCTGAGTCAGGAGTTTGAGACCA	17549
Db	27539	ATCCAGCACTTTGGGAGGCGAGGTGGCGAGATCACCTGAGTCAGGAGTTTGAGACCA	27480
QY	17550	GCCTGGCCAAATCGGAAATCCCGTCTCTACTAAAAATACAAAAATTTAGCCGAGCTGGT	17609
Db	27479	GCCTGGCCAAATCGGAAATCCCGTCTCTACTAAAAATACAAAAATTTAGCCGAGCTGGT	27420
QY	17610	ACAGGACCTGTAAATCCAGCTGTTTCAAGTGGCTGAGTCAGAGATAGCCTGGATCCGG	17669
Db	27419	ACAGGACCTGTAAATCCAGCTGTTTCAAGTGGCTGAGTCAGAGATAGCCTGGATCCGG	27360
QY	17670	GAGTGGAGTTTGTAGTAAAGCAAGATTGGCCATTCGATGCGAGCTGGCGGACAGAGC	17729
Db	27359	GAGTGGAGTTTGTAGTAAAGCAAGATTGGCCATTCGATGCGAGCTGGCGGACAGAGC	27300
QY	17730	AGACTTTTCTTAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC	17789
Db	27299	AGACTTTTCTTAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC	27240
QY	17790	AAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17849
Db	27239	AAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	27180
QY	17850	AGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	17909
Db	27179	AGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	27120
QY	17910	GAAAGAAATACCTCCAGAGAGCCAGGTCCTTTAGGCCCTCTTGAGAACTCACATCCCTT	17969
Db	27119	GAAAGAAATACCTCCAGAGAGCCAGGTCCTTTAGGCCCTCTTGAGAACTCACATCCCTT	27060
QY	17970	TTGATGAACACAAATGCTTCACTCTCAATGTTTATTTGGTAAATCCAAGTTTCAATATAC	18029
Db	27059	TTGATGAACACAAATGCTTCACTCTCAATGTTTATTTGGTAAATCCAAGTTTCAATATAC	27000
QY	18030	CTAAATCACTTAGTACTGAATCTGGCATATAGTAAATCACCTTAATGAAGAGATAAGAGTCA	18089
Db	26999	CTAAATCACTTAGTACTGAATCTGGCATATAGTAAATCACCTTAATGAAGAGATAAGAGTCA	26940
QY	18090	TGGAGTATTCGAAGCAATTAAGATCAATAGACTCAATATACATGGCAACAAAGTTGG	18149
Db	26939	TGGAGTATTCGAAGCAATTAAGATCAATAGACTCAATATACATGGCAACAAAGTTGG	26880
QY	18150	ATCTTAAAAACCGACCTGAGTGAAGAAAGAAAGGAAAGATACATAACACGGTACCATTA	18209
Db	26879	ATCTTAAAAACCGACCTGAGTGAAGAAAGAAAGGAAAGATACATAACACGGTACCATTA	26820
QY	18210	TGTAATTTGAATAATATATGCTTACAAATTTGTAAGAACACATACAAATAGATACATGTA	18269
Db	26819	TGTAATTTGAATAATATATGCTTACAAATTTGTAAGAACACATACAAATAGATACATGTA	26760
QY	18270	TATTAATATATCTCGAAGCGTTA-CCTATGGGTGGTGGCTGGAGTGGGGTAAAGTCCT	18328
Db	26759	TATTAATATATCTCGAAGCGTTA-CCTATGGGTGGTGGCTGGAGTGGGGTAAAGTCCT	26700
QY	18329	AAGCTGTAATGGAACCTTAAACAAATACATGAAACGAGTAGGAATCAGAAAGAGTAACAAT	18388
Db	26699	AAGCTGTAATGGAACCTTAAACAAATACATGAAACGAGTAGGAATCAGAAAGAGTAACAAT	26640
QY	18389	AAAAATGTCATGAACGAGGAGTGAATTAATTAATCACTCACTGCATCTGAGGTTAAAA	18448
Db	26639	AAAAATGTCATGAACGAGGAGTGAATTAATTAATCACTCACTGCATCTGAGGTTAAAA	26580
QY	18449	ATAGAAAGATGAATTTGTTATTTCTTATTTACTCTAGGTCTTCCACTTGCACCTCAGCTTT	18508
Db	26579	ATAGAAAGATGAATTTGTTATTTCTTATTTACTCTAGGTCTTCCACTTGCACCTCAGCTTT	26520
QY	18509	ACAAATGTTGGACTATCCTTCAGATGGCAACCTCCTTGCACTTGTCTAGGCGAGGAGCTT	18568
Db	26519	ACAAATGTTGGACTATCCTTCAGATGGCAACCTCCTTGCACTTGTCTAGGCGAGGAGCTT	26460
QY	18569	TTTCCTCCAGCTTTCTAGGTGATTTAATATATCAGGGAATAAGTATAAAAAGGACGCG	18628
Db	26459	TTTCCTCCAGCTTTCTAGGTGATTTAATATATCAGGGAATAAGTATAAAAAGGACGCG	26400
QY	18629	TGCTCCCTGGGTAGCTTTCTGGACTTCAGAGCTTAAATTCGAAAGTCAGTTTTACACATG	18688
Db	26399	TGCTCCCTGGGTAGCTTTCTGGACTTCAGAGCTTAAATTCGAAAGTCAGTTTTACACATG	26340
QY	18689	TGATTTTCATCTGAATTAAGGCAAGTAGAATACTGGCAGACAGAAAAAATGTGATTTAT	18748
Db	26339	TGATTTTCATCTGAATTAAGGCAAGTAGAATACTGGCAGACAGAAAAAATGTGATTTAT	26280
QY	18749	TATGGTGTACTATCCCTTACAGCGGAGTGTACGCTGCTCTTTTGTCCACTGATTTA	18808
Db	26279	TATGGTGTACTATCCCTTACAGCGGAGTGTACGCTGCTCTTTTGTCCACTGATTTA	26220
QY	18809	AGGCAAGATGAACGAAAGTGGCTATGATCAGTCTTTCAAAGACACACTCTGGCCCCCTCG	18868
Db	26219	AGGCAAGATGAACGAAAGTGGCTATGATCAGTCTTTCAAAGACACACTCTGGCCCCCTCG	26160

QY 27472 TCATCTCAAGCTTAAATAATTTAAATGGGCGCAGGCGAGTGGCTCACATCTGTATATCCC 27531
DB 17402 TCATCTCAAGCTTAAATAATTTAAATGGGCGCAGGCGAGTGGCTCACATCTGTATATCCC 17343
QY 27532 AGCATTTTGGGAGGCAAGGGGGGGTGTATCACTTTGAGGTTCAGAGTTCAGACCGAGCT 27591
DB 17342 AGCATTTTGGGAGGCAAGGGGGGGTGTATCACTTTGAGGTTCAGAGTTCAGACCGAGCT 17283
QY 27592 GGCACACATGGGAAACCCCTCTCTCAAAAAAGTATAAAAGTTAAACAGGTCGTGGAG 27651
DB 17282 GGCACACATGGGAAACCCCTCTCTCAAAAAAGTATAAAAGTTAAACAGGTCGTGGAG 17223
QY 27652 CATTTGCTGTGGTCCCACTACTCAGAGGCTCAGAGCGAGGAAATCAGCTTTAATCTGGG 27711
DB 17222 CATTTGCTGTGGTCCCACTACTCAGAGGCTCAGAGCGAGGAAATCAGCTTTAATCTGGG 17163
QY 27712 AGGTGGAGTTGAGTGAGCCAGATCTCTCACTGCACTCCAGCCTGGGTGACAGCA 27771
DB 17162 AGGTGGAGTTGAGTGAGCCAGATCTCTCACTGCACTCCAGCCTGGGTGACAGCA 17103
QY 27772 AGACTCTATCTCAAAACAAACATTAACAAACAAACAAACATTTAAATGGCTGCACTT 27831
DB 17102 AGACTCTATCTCAAAACAAACATTAACAAACAAACAAACATTTAAATGGCTGCACTT 17043
QY 27832 GCTCTGAAAAATGATTTCTTTGGCCAGATGTGTGCTCAAACTGTAAATCCCAACT 27891
DB 17042 GCTCTGAAAAATGATTTCTTTGGCCAGATGTGTGCTCAAACTGTAAATCCCAACT 16983
QY 27892 TTGGGAAGCTAAGGCGAGGAGTTCGAGACGAGTTCAGGATATAGGAAGACAACTCTCT 27951
DB 16982 TTGGGAAGCTAAGGCGAGGAGTTCGAGACGAGTTCAGGATATAGGAAGACAACTCTCT 16923
QY 27952 ACAAAAAAATCCAAAAATTTAGTCAAGGCTTATTTGTTATGCTGTAGTCCAGGTACT 28011
DB 16922 ACAAAAAAATCCAAAAATTTAGTCAAGGCTTATTTGTTATGCTGTAGTCCAGGTACT 16863
QY 28012 CAGGAGGCTGAGGAGGAGTTCCTCAAGCCAGGAGTTCAGGATATAGGAAGACAACTCTCT 28071
DB 16862 CAGGAGGCTGAGGAGGAGTTCCTCAAGCCAGGAGTTCAGGATATAGGAAGACAACTCTCT 16803
QY 28072 GCACAACTGCACTCCATCTTGGGTGACAGACAGGTCCTATCTCTGGAG-AAAAAATA 28130
DB 16802 GCACAACTGCACTCCATCTTGGGTGACAGACAGGTCCTATCTCTGGAG-AAAAAATA 16743
QY 28131 AAAAGAGGCAATTTCTTAGGAGAGTTCCTCTGAGAGGTCCTAAGGTTCCATGGAAT 28190
DB 16742 AAAAGAGGCAATTTCTTAGGAGAGTTCCTCTGAGAGGTCCTAAGGTTCCATGGAAT 16683
QY 28191 CCTTAAAGCATCAGAGTATGTAGTCAATGGGAGGAGCATTTAGCCAGAGCAGTTCT 28250
DB 16682 CCTTAAAGCATCAGAGTATGTAGTCAATGGGAGGAGCATTTAGCCAGAGCAGTTCT 16623
QY 28251 GCTCCCATGCAATTAATTTTAAAAACAAAGCTATATAAAGTTTGAAGTCTACTA 28310
DB 16622 GCTCCCATGCAATTAATTTTAAAAACAAAGCTATATAAAGTTTGAAGTCTACTA 16563
QY 28311 CGTAGCATCAGCCTGACATTTAATGCTCGTAAATCAAACTTAATGACTTTTAGC 28370
DB 16562 CGTAGCATCAGCCTGACATTTAATGCTCGTAAATCAAACTTAATGACTTTTAGC 16503
QY 28371 CAGTTATGCTACTAGCCACTACAGACACACACTTTTAAACAAATTTAGACTAATAGTT 28430
DB 16502 CAGTTATGCTACTAGCCACTACAGACACACACTTTTAAACAAATTTAGACTAATAGTT 16443
QY 28431 GTCATCAGTGAATCAAGTTTGGCATTTCTCAATGCTTTGCTCACAACATTAATCTTT 28490
DB 16442 GTCATCAGTGAATCAAGTTTGGCATTTCTCAATGCTTTGCTCACAACATTAATCTTT 16383
QY 28491 CTGGAATGCTGCTGACTCATCTCTGTTGTAACCTTATACCCAACTTTAAAAACCTAG 28550
DB 16382 CTGGAATGCTGCTGACTCATCTCTGTTGTAACCTTATACCCAACTTTAAAAACCTAG 16323
QY 28551 CTCAGAGTTCAACTCCCATTCATTTCAAAAAAGAGCTTCTCTCTCTTAAAGTTTAA 28610

DB 16322 CTCAGAGTTCAACACATTCATTCATTTCAAAAAGAGCTTCTCTCTCTTAAAGTTTAA 16263
QY 28611 GAACTCATTTTCAATGAACTTTTGGCATTTATGACACATGCTGCTGCTGTTGTTATTT 28670
DB 16262 GAACTCATTTTCAATGAACTTTTGGCATTTATGACACATGCTGCTGCTGTTATTT 16203
QY 28671 GTGTTCAGCTCATATGCCCCCAAGGTTTGTAGTCTCTTAAACGGAATAATGATGCT 28729
DB 16202 GTGTTCAGCTCATATGCCCCCAAGGTTTGTAGTCTCTTAAACGGAATAATGATGCT 16143
QY 28730 CTAACACCTTTCTATCTTTTCAATGCTTCTAGTCTGTTGTTGCTTATAAAGAAATAC 28789
DB 16142 CTAACACCTTTCTATCTTTTCAATGCTTCTAGTCTGTTGTTGCTTATAAAGAAATAC 16083
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DB 16082 CTGAGGCTGGGGAATTTATTTAAAAAGAGGTTTATTTGGCTCAGATTCGCA-GCTAT 16023
QY 28849 ATAAGAGCATAGTGTGAGCATCTGCTTCAAGGTGAGGCTTCAGGAAGTTTCCACCCATG 28908
DB 16022 ATAAGAGCATAGTGTGAGCATCTGCTTCAAGGTGAGGCTTCAGGAAGTTTCCACCCATG 15963
QY 28909 GTAGAGGCAAGGAGGAGCAGGATCAGATATCAAGAGAGGAGGAAAAAAGGAAGGAAG 28968
DB 15962 GTAGAGGCAAGGAGGAGCAGGATCAGATATCAAGAGAGGAGGAAAAAAGGAAGGAAG 15903
QY 28969 AAGGAGGCTGCCATTTCTTTCAACAATCAGTTCTTTGGGAACTTAATGGGACAAAGAGG 29028
DB 15902 AAGGAGGCTGCCATTTCTTTCAACAATCAGTTCTTTGGGAACTTAATGGGACAAAGAGG 15843
QY 29029 CTGGGCAAGTGTGCTGATGCTGTAATCCAGCCCTTTGGGAGACAAAGGTGGTGGATC 29088
DB 15842 CTGGGCAAGTGTGCTGATGCTGTAATCCAGCCCTTTGGGAGACAAAGGTGGTGGATC 15783
QY 29089 ACCTGAAGTCAGAAAGCTCAGACAGCAGCTGGCAATGTGTTGAACTCCGCTCTACTAA 29148
DB 15782 ACCTGAAGTCAGAAAGCTCAGACAGCAGCTGGCAATGTGTTGAACTCCGCTCTACTAA 15723
QY 29149 AATATCAAAAATTTAGTGGGCTGGTGGTGTATCCTGTAGTCCAGATATCTCAGGAGC 29208
DB 15722 AATATCAAAAATTTAGTGGGCTGGTGGTGTATCCTGTAGTCCAGATATCTCAGGAGC 15663
QY 29209 TGAGTGGAGTAACTTCTTGAACCCGGAAGACAGAGGTTGCACTGAGCTGAGATTTGCTCC 29263
DB 15662 TGAGTGGAGTAACTTCTTGAACCCGGAAGACAGAGGTTGCACTGAGCTGAGATTTGCTCC 15603
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DB 15302 GGTGCTAGTACTGCTTCTGCAAAAAGGAGAAAAAATTTGATAGTCACTGTTTGTGTGTG 15243
QY 29624 TGTGTGTTTATGTAAAGAGATCAAGAGAAAGAAACAAAGAAATCTATGAAAGAGGAGG 29683

Dd	10857	TGGGCTCCAGAGGCGAAGAGGACGTTGAAGGGAATGGGAGTGGGTGAATATATAGAC	10808
Qy	34059	GATGGGGACCAACCAAGACAGTCCGCTATTGCAAAACTGAGGAGAGAGAGTCTGGAGG	34118
Dd	10807	GATGGGGACCAACCAAGACAGTCCGCTATTGCAAAACTGAGGAGAGAGAGTCTGGAGG	10748
Qy	34119	GGGTGGTGGAGCTGGGTCTCCTTAAGAGGTTTTTGACAAAGCAGTCAATGGACGGGCT	34178
Dd	10747	GGGTGGTGGAGCTGGGTCTCCTTAAGAGGTTTTTGACAAAGCAGTCAATGGAGCGGCT	10688
Qy	34179	TAGAAATCACAGTTGGGACAGGCTAAAGTTCTCTCGGGATATAGAGATGAGATTAGAAG	34238
Dd	10687	TAGAAATCACAGTTGGGACAGGCTAGATTCTCTCGGGATATAGAGATGAGATTAGAAG	10628
Qy	34239	AGTTTCCAACTAGGGTATGTGGGAAAAAGCACTATTGACCCAAAAAGGAGAGAAATGT	34298
Dd	10627	AGTTTCCAACTAGGGTATGTGGGAAAAAGCACTATTGACCCAAAAAGGAGAGAAATGT	10568
Qy	34299	GGGTGGAGTGGCAGAGAAAGAGGGTTTGAGCAGAGAGTGGTGAATTTCTTAATGCAGA	34358
Dd	10567	GGGTGGAGTGGCAGAG- AAGAGGGTTTTGAGCAGAGAGTGGTGAATTTCTTAATGCAGA	10509
Qy	34359	GTGTGGAGGTGGAGTGCAGGAGCCAGGCTGGGTGGCTGTGCTGATGTGATTAAGCAC	34418
Dd	10508	GTGTGGAGGTGGAGTGCAGGAGCCAGGCTGGGTGGCTGTGCTGATGTGATTAAGCAC	10449
Qy	34419	TTACTGACTGCCAGGCAATGGCTAAGTACTCAGATGCTTTGTCTGTTATCCCTCCGAC	34478
Dd	10448	TTACTGACTGCCAGGCAATGGCTAAGTACTCAGATGCTTTGTCTGTTATCCCTCCGAC	10389
Qy	34479	AACCCCTCTGA- GCAGTGCAGTATTATTCTCACTTCACAGATAAGGAAATTTGAGGCAC	34537
Dd	10388	AACCCCTCTGAGCAGGTGCAGTTATTATTCTCACTTCACAGATAAGGAAATTTGAGGCAC	10329
Qy	34538	AGAGAA-TTGAAGTAACTTACCAAGGTGACATAGCTCATATATGGTAAAGCAGGCTTTGA	34596
Dd	10328	AGAGAA-TTGAAGTAACTTACCAAGGTGACATAGCTCATATATGGTAAAGCAGGCTTTGA	10269
Qy	34597	ACTCAGTCTAGCTCCCGAAGCTAAGCTTGTAATCTACTATGCTTTTCCCAAAAAGGGGG	34656
Dd	10268	ACTCAGTCTAGCTCCCGAAGCTAAGCTTGTAATCTACTATGCTTTTCCCAAAAAGGGGG	10209
Qy	34657	CTGGCAAAAAGAGCTGA- GGGGGCTGGGCATGCTGGCTCATGCTGTAATCCCAGCAC	34715
Dd	10208	CTGGCAAAAAGAGCTGAGGGGGCTGGGCATGCTGGCTCATGCTGTAATCCCAGCAC	10149
Qy	34716	TTCCGGAGACTGAGGAGGCTGGTTCACAGAGTTCCAGAGTTCCAGACCAAGCTGGTCAA	34775
Dd	10148	TTCCGGAGACTGAGGAGGCTGGTTCACAGAGTTCCAGAGTTCCAGACCAAGCTGGTCAA	10089
Qy	34776	CATGGTGAAGCCCTGCTCTACTTAAATAACAAAAATAGCTGGGTGGTGGTGTGTCAC	34835
Dd	10088	CATGGTGAAGCCCTGCTCTACTTAAATAACAAAAATAGCTGGGTGGTGGTGTGTCAC	10029
Qy	34836	CTGTAGTCCAGCTACTTTGGGAGGCTGAGGAGAGATGCGCTTGAAACCCAGAGGGGG	34895
Dd	10028	CTGTAGTCCAGCTACTTTGGGAGGCTGAGGAGAGATGCGCTTGAAACCCAGAGGGGG	9969
Qy	34896	ATGTTGTAGTGACCAAGATCATGCCACTGGACTCCAGCTCCAGCTGGGTGACAGCTGAGCTC	34955
Dd	9968	ATGTTGTAGTGACCAAGATCATGCCACTGGACTCCAGCTCCAGCTGGGTGACAGCTGAGCTC	9909
Qy	34956	CATCCAAAAAAGAGAGCTGAGGTGATGGCCACCATCAGCATCAGCCTGGAAGTTATA	35015
Dd	9908	CATCCAAAAAAGAGAGCTGAGGTGATGGCCACCATCAGCATCAGCCTGGAAGTTATA	9849
Qy	35016	GCAGGATGCTAAGTTTCTTAAGCTGCTTTCTTAGGACTTGAAGATTAACCTGGGT	35075
Dd	9848	GCAGGATGCTAAGTTTCTTAAGCTGCTTTCTTAGGACTTGAAGATTAACCTGGGT	9789
Qy	35076	TTGTATCCCATCTCTGCCATTAGTATTACTGGCTTTGGATAAATTTACTTAGCCCTACT	35135
Dd	9788	TTGTATCCCATCTCTGCCATTAGTATTACTGGCTTTGGATAAATTTACTTAGCCCTACT	8649
Qy	35136	GAACCAACTTTGGATTTTATATAGATACTGTAAATGAAGGAATAGGTATCAGTCTTAG	35195
Dd	9728	GAACCAACTTTGGATTTTATATAGATACTGTAAATGAAGGAATAGGTATCAGTCTTAG	9669
Qy	35196	CAGAGCATCCAGAGTGTCTTATTAACCACTAAATCATATCCTGTTCATTCGCTCCGCCA	35255
Dd	9668	CAGAGCATCCAGAGTGTCTTATTAACCACTAAATCATATCCTGTTCATTCGCTCCGCCA	9609
Qy	35256	AACCAATTCAATGGCTTCCCACTCAAGTTTAAACCTCAATCTTTCCAGTGGCTCAAGA	35315
Dd	9608	AACCAATTCAATGGCTTCCCACTCAAGTTTAAACCTCAATCTTTCCAGTGGCTCAAGA	9549
Qy	35316	GGCTATGCTATCCGGTGTCTGACCTCATCTGTGTGTTCTTTCTCCCTCCCTTTCTGGCT	35375
Dd	9548	GGCTATGCTATCCGGTGTCTGACCTCATCTGTGTGTTCTTTCTCCCTCCCTTTCTGGCT	9489
Qy	35376	CAGAGCAGCATCTGTCTCTCTGCTGCTTGAATAACAGGAGCAGCTCTCTTCGCT	35435
Dd	9488	CAGAGCAGCATCTGTCTCTCTGCTGCTTGAATAACAGGAGCAGCTCTCTTCGCT	9429
Qy	35436	GAACCACTTTACCCAGATATCTTAGCTTACTCTCTGCTCCCTCAATCTTAATGATGAA	35495
Dd	9428	GAACCACTTTACCCAGATATCTTAGCTTACTCTCTGCTCCCTCAATCTTAATGATGAA	9369
Qy	35496	TGTCTCAGTGAAGTCTTCTCTCTCTCTCTGCTTAAAGTATATCTCTCTTCCCTTTCTTT	35555
Dd	9368	TGTCTCAGTGAAGTCTTCTCTCTCTCTCTGCTTAAAGTATATCTCTCTTCCCTTTCTTT	9309
Qy	35556	ACTGTTCTAGCTACTATTGCTGTGTAAACATCTCCCAAAATTAATGATGAAACA	35615
Dd	9308	ACTGTTCTAGCTACTATTGCTGTGTAAACATCTCCCAAAATTAATGATGAAACA	9249
Qy	35616	TCAGCCATCATCTTATTTCTCAGGTTTCTCAGGTTGAGGAGTCAAGGAGTCAAGTCA	35675
Dd	9248	TCAGCCATCATCTTATTTCTCAGGTTTCTCAGGTTGAGGAGTCAAGGAGTCAAGTCA	9189
Qy	35676	GGGAGTTCTGGCTCTATATCTCTTATGCTGAGAGTCAAGTCAAGTCAAGTCAAGTCA	35735
Dd	9188	GGGAGTTCTGGCTCTATATCTCTTATGCTGAGAGTCAAGTCAAGTCAAGTCAAGTCA	9129
Qy	35736	ACAAAGCAGGTTCTTAGTGTGAGGCTGGCTGGCTCTCTCAGATATAGTTCAGATCTC	35795
Dd	9128	ACAAAGCAGGTTCTTAGTGTGAGGCTGGCTGGCTCTCTCAGATATAGTTCAGATCTC	9069
Qy	35796	CTCAGGGGGTCTCTCCAGTGGCTAGTCTGAACTTCTCAGAGTGGTGGCTCAGG	35855
Dd	9068	CTCAGGGGGTCTCTCCAGTGGCTAGTCTGAACTTCTCAGAGTGGTGGCTCAGG	9009
Qy	35856	GCAGTGGAGCTCTGATAGTGGCTGAGGCTTCCAGCTGAGTATTCAGAGCAAGAGTG	35915
Dd	9008	GCAGTGGAGCTCTGATAGTGGCTGAGGCTTCCAGCTGAGTATTCAGAGCAAGAGTG	8949
Qy	35916	GGAGCTGTATTGCTCTATATGACCCAACTTGAATCCACAGCATCAGTTCGCTGTAT	35975
Dd	8948	GGAGCTGTATTGCTCTATATGACCCAACTTGAATCCACAGCATCAGTTCGCTGTAT	8889
Qy	35976	TCTACGGGTTGAAAGTCAAAAACCAACAGTTTCAAGAGAGAGAAACAGATCACA	36035
Dd	8888	TCTACGGGTTGAAAGTCAAAAACCAACAGTTTCAAGAGAGAGAAACAGATCACA	8829
Qy	36036	TTTCTCAATTGGAGAGGTTCAAGTCAATGTAATCAGAGCTATGGGATACGAAGTA	36095
Dd	8828	TTTCTCAATTGGAGAGGTTCAAGTCAATGTAATCAGAGCTATGGGATACGAAGTA	8769
Qy	36096	TTGGGTCAGGTATGAAAAATTTGATTTGCTGATCTGCTTTACTTTCTCCAGCGCTTC	36155
Dd	8768	TTGGGTCAGGTATGAAAAATTTGATTTGCTGATCTGCTTTACTTTCTCCAGCGCTTC	8709
Qy	36156	ATGATCTGCTTCCACATGATATTGCTTACGTCATTTCTCGGTTTCTCTTCCACAC	36215
Dd	8708	ATGATCTGCTTCCACATGATATTGCTTACGTCATTTCTCGGTTTCTCTTCCACAC	8649

Db 3917 GACATTCAGAGTCTAGTCTCTTAATAGCTTTGTAGTCTCTTAACAGCTTTTTCATTC 3976
Qy TTGCTCTGTGTTTGTATTTCTTGATGATGCCAAATATTCCTGTAAATAAATCTTA 5443
Db 3977 TTGCTCTGTGTTTGTATTTCTTGATGATGCCAAATATTCCTGTAAATAAATCTTA 4036
Qy 5444 GATAAGTCATCTCTATCCAGAAATAGGCACATTTTGTGTCAGTCATAGTGTGA 5503
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1 (bases 1 to 100020)
Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
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2 (bases 1 to 100020)
Abbott, S. and Haglund, K.
The sequence of Homo sapiens BAC clone RP11-753F4
Unpublished (2001)
3 (bases 1 to 100020)
Waterston, R.H.
Direct Submission
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 100020)
Waterston, R.H.
Direct Submission
Submitted (04-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 100020)
Waterston, R.
Direct Submission
Submitted (21-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 4, 2002 this sequence version replaced gi:17981677.
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Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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Summary Statistics
Center project name: H_NH0753F04
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frenken, E., Taten, M., Catane, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-762N20, 2000 bp overlap; the clone sequenced to the right is RP11-485D7. Actual start of this clone is at base position 98039 of RP11-762N20; actual end is at base position 100020 of RP11-753F4.

Data from AC09338 and AC074188 was used to finish this clone, AC092165. Polymorphisms have been identified between AC074188 and AC092165.

FEATURES

source

Location/Qualifiers
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LOCUS      Homo sapiens clone RP11-91N19, WORKING DRAFT SEQUENCE, 15 unordered
DEFINITION      pieces.
AC012033
VERSION      AC012033.20 GI:9966196
KEYWORDS      HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158276)
Muzny,D.M., Adams,C., Bailey,M., Barberia,J., Blankenburg,K.,
Bodera,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N.,
Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferriguccio,D.,
Forcum-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L.,
Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,
Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M.,
Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z.,
Lichtarge,O., Liu,J., Liu,W., Logan,O., Lozado,R.J., Lu,J.,
Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Morgan,M.,
Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S.,
Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L.,
Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S.,
Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sugeng,R.,
Tabors,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wabnah,M.,
Watlington,S., Weinstock,G., Weinstock,I.R., Williamson,A.,
Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D., and
Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 158276)
Worley,K.C.
Direct Submission
Submitted (19-OCT-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 4, 2000 this sequence version replaced gi:9929521.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HMOR
Center clone name: RP11-91N19
----- Summary Statistics
Assembly program: Phrap; version 0.950329
Consensus quality: 13597 bases at least Q40
Consensus quality: 14594 bases at least Q30
Consensus quality: 149762 bases at least Q20
Estimated insert size: 149948; sum-of-contigs estimation
Estimated insert size: 249006; agarose-fp estimation
Quality coverage: 2.8x in Q20 bases; agarose-fp estimation
Quality coverage: 4.6x in Q20 bases; sum-of-contigs estimation
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1
* 44367: contig of 44367 bp in length
* 44368: gap of unknown length
* 73078: contig of 28611 bp in length
* 73079: gap of unknown length
* 73179: contig of 21028 bp in length

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* 94207 94306: gap of unknown length
* 94307 112788: contig of 18482 bp in length
* 112889 112888: gap of unknown length
* 112889 120123: contig of 7435 bp in length
* 120423 120423: gap of unknown length
* 120424 130440: contig of 10017 bp in length
* 130441 130540: gap of unknown length
* 130541 135818: contig of 5278 bp in length
* 135819 135918: gap of unknown length
* 135919 141234: contig of 5316 bp in length
* 141235 141334: gap of unknown length
* 141335 145332: contig of 3898 bp in length
* 145333 145332: gap of unknown length
* 145333 149660: contig of 4328 bp in length
* 149661 149760: gap of unknown length
* 149761 150931: contig of 1171 bp in length
* 150932 151031: gap of unknown length
* 151032 152757: contig of 1726 bp in length
* 152758 152857: gap of unknown length
* 152858 154933: contig of 2076 bp in length
* 154934 155033: gap of unknown length
* 155034 156717: contig of 1884 bp in length
* 156718 156817: gap of unknown length
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Matches 1889; Conservative 0; Mismatches 411; Indels 226; Gaps 21;
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DB 109889 ACCTTAATTTTAAAGTCTTTTATTAATAAAAAATGCTAAACAATC-ATTGAGCATTCAGT 109948
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DB 109949 GAGTCGTACTCTTTTCTGCTGGAGGCTCTTGCTCGAGGTTGATGTTGCTGACTGGT 110008
QY 1276 -CGGGGGTCAAGTCTGAAGCTTAGGGTGGCTGGCAGTTTCTTAAA---ACAACAG 1329
DB 110009 CAGGGTGGTGGCTGCTGAAGGTTGGGGTGGCTGGCAATTTCTTAATAAAGACATCGG 110068
QY 1330 TGAAGATTGAATATACAGTTGACCTTTCCTTTCATGAAGAAATTTCTCTAGTGTGTGAT 1389
DB 110069 TGAAGCTTTTGGCATGAGTTGACTCTTCTTTCATGAAGAAATTTCTCTAGTGTGTGAT 110128
QY 1390 GCTTTTGTATGAGCATTTTATGACAGTAGAACTCTTTTGAATAATGGA-TCAATCCTCTC 1448
DB 110129 GCTGTTTGTATGAGCATTTTGTCCACAGTAGAGTCTTTTCAAAATGGAGTCAATCCTCTC 110189
QY 1449 AAACCCCTGCTGCTTTTAAACAACCTAAGTTAATAATATATTCGAATCCCAATGTTGTCAT 1508
DB 110189 AAACCCCTGCTGCTTTATCAACTAAGTTATGTAATATTCCTTAAATCCCTTTGTTGTCAT 110248
QY 1509 TTCAACAATTTTCAAGTGTCTTCAACAGGAGTAGATTTCCATCTCATTTCTCTGAGATGGA 1568
DB 110249 TTCAACAATGTTCAAGCATCTTTCACAGGTTAGATTCATCTCTCAAGAAACCACTT--- 110305
QY 1569 ATCTTTGCTCATCCATAAGAAAGAAATTCCTCATCTGTTCAAGTTTATCATGAGATGGA 1628

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Db 110365 GCAATACAGTCATGCTTCCAGGCTCAGTCTCACTTTTAAATCCAGTCTCTGCTGTTTC 110419
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Db 110420 CACCACATCTGCACTTCTTCCACTGAAGTCTGAACTCTCCAGTCAATCATGAG 110479
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Db 110480 GGTGGAATCAACTTCTCCAAACTCCTGTTAAATTTGAATTTGAACCTCTCCCATGA 110539
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Db 110540 ATCAGGAATGTTTAAATGCGATCTAAATGCTGAACTCTTCCAAAGGTTTCAATTT 110599
Qy 1866 ACTTAGTCAGATCCATCCATCCAGAGATCCACTTTCAATGCCAGTTATGCCATTAGG 1925
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Qy 1986 AATAGATGTTGTTAGCAGCATGAAGCAACATTAATCTTTTGTACATGTCATC 2045
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Qy 2046 AGAGCTCTGGTGACAGATATTTGCCAGTCAAGTAAATTAATCTTTTGAAGGAAT-TAT 2104
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Db 111075 CCAGCACTGATCTCTCTAGCTATGAAGTTCTAGATGCACTTCTTCCCAATAG 111134
Qy 2404 AAGCTGTTTATCTAATGAATACTGTTTGTAGTATGAGCAGCTTCAATCAATGATA 2463
Db 111135 AAGCTGTTTATCTAATGAATACTGTTTGTAGTATGAGCAGCTTCAATCAATGATA 111194
Qy 2464 CTATCTAGATCTCTTGGATACTTG-TGCAGCTTCTACATCAGCATTTGCTACCTTCACT 2522
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Qy 3058 TCTTGGATGACAGAGCAAGACCTTTCTCAAAATAAAATGAGAGGTTGTCTTCTTTT 3117
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Qy 3118 GTTTGAGCCATAGAACCCATAGTATGATTTTAAATGCGCTAATTTCAATCTGTTGTG 3177
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Qy 3298 TGATGCCCCCAACCAATTAAGATTAATTAAGCAATTAATTAATTAATTAATTAATTAATTAAT 3357
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RESULT 13

AC074188 179816 bp DNA linear HTG 21-FEB-2001
LOCUS Homo sapiens chromosome 2 clone RP11-341G20, WORKING DRAFT
DEFINITION SEQUENCE, 17 unordered pieces.
AC074188
AC074188.3 GI:13027574
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179816)
Waterston,R.H.
The sequence of Homo sapiens clone
2 (bases 1 to 179816)
Waterston,R.H.
Direct Submission
Submitted (16-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Feb 21, 2001 this sequence version replaced gi:9802849.

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
----- Project Information -----
Center project name: H_NH0341G20
----- Summary Statistics -----
Sequencing vector: M13, 94%
Chemistry: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 167169 bases at least Q40
Consensus quality: 170689 bases at least Q30
Consensus quality: 172797 bases at least Q20
Insert size: 186000; agarose-fp
Quality coverage: 5.07 in Q20 bases; sum-of-contigs
Quality coverage: 5.39 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
consists of 17 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 3838: contig of 3838 bp in length
3839 3938: gap of unknown length
3939 9357: contig of 5429 bp in length
9358 9457: gap of unknown length
9458 15261: contig of 5794 bp in length
15262 15361: gap of unknown length
15362 21615: contig of 6254 bp in length
21616 21715: gap of unknown length
21716 28467: contig of 6752 bp in length
28468 28567: gap of unknown length
28568 36770: contig of 8203 bp in length
36771 36870: gap of unknown length
36871 48944: contig of 12074 bp in length
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60730 60830: gap of unknown length
60831 74071: contig of 13242 bp in length
74072 74171: gap of unknown length
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101608 101707: gap of unknown length
101708 120321: contig of 18514 bp in length
120322 124319: gap of unknown length
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144720 172326: contig of 27607 bp in length
172327 172426: gap of unknown length
172427 174046: contig of 1620 bp in length
174047 176137: contig of 1991 bp in length
176138 176137: contig of 1991 bp in length

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

* 176138 176237: gap of unknown length
* 176238 179816: contig of 3579 bp in length.
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Matches 1889; Conservative 0; Mismatches 411; Indels 226; Gaps 21;
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Qy 1276 -CGGGGTGAGTCTGAGACCTTAGGTTGGCTGTGGCAGTTCTTCTTAA-----ACAACAG 1329
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Db      151915 AGGGTGCACAAACCTCCATTTGTTTTCAGATGCCCTATCTGCGAAGCGTAATAAA 151974
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RESULT 14
BC035143/c
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DEFINITION Homo sapiens cDNA clone MGC:43254 IMAGE:5264460, complete cds.
ACCESSION BC035143
VERSION    BC035143.1 GI:3243251
KEYWORDS   MGC.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2641)
            Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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            Bouffard,G.C., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
            Genation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
            Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)
            12477932
            2 (bases 1 to 2641)
            Strausberg,R.
            Direct Submission
            Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: cgabbs@mail.nih.gov
            Tissue procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Institute for Systems Biology
            http://www.systemsbio.org
            contact: anadan@systemsbiology.org
            Anup Madan, Jessica Fahay, Erin Heiton, Mark Kettman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAC plate: 73 Row: j Column: 13
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 22209000.
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               /db_xref="taxon:9606"
               /clone="MGC:43254 IMAGE:5264460"
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FEATURES             source

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CDS

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GSD"
780. .896
/notes="CENP-B_N; Region: CENP-B N-terminal DNA-binding
domain. Centromere Protein B (CENP-B) is a DNA-binding
protein localised to the centromere. Within the N-terminal
125 residues, there is a DNA-binding region, which binds
to a corresponding 17bp CENP-B box sequence. CENP-B dimers
either bind two separate DNA molecules or alternatively,
they may bind two CENP-B boxes on one DNA molecule, with
the intervening stretch of DNA forming a loop structure.
The CENP-B DNA-binding domain consists of two repeating
domains, RP1 and RP2. This family corresponds to RP1 has
been shown to consist of four helices in a
helix-turn-helix structure"
/db_xref="CDD:pfam04218"
939. .1151
/notes="CENPB; Region: Putative DNA-binding domain in
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/db_xref="CDD:smart00674"
1206. .1931
/notes="DDE; Region: DDE superfamily endonuclease. This
family of proteins are related to pfam00665 and are
probably endonucleases of the DDE superfamily. Transposase
proteins are necessary for efficient DNA transposition.
This domain is a member of the DDE superfamily, which
contain three carboxylate residues that are believed to be
responsible for coordinating metal ions needed for
catalysis. The catalytic activity of this enzyme involves
DNA cleavage at a specific site followed by a strand
transfer reaction. Interestingly this family also includes
the CENP-B protein. This domain in that protein appears to
have lost the metal binding residues and is unlikely to
have endonuclease activity. Centromere Protein B (CENP-B)
is a DNA-binding protein localised to the centromere"
/db_xref="CDD:pfam03184"

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ORIGIN

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Query Match      3.0%; Score 1204.8; DB 9; Length 2641;
Best Local Similarity 74.9%; Pred. No. 1e-204;
Matches 1871; Conservative 0; Mismatches 402; Indels 225; Gaps 20;

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Db      |||||
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Db      |||||
Qy 2563 GCAATAGCATTTGCTATAATAAACAAATATACATACCTAAATTTTAAATGCTTTTACTA 2504
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Qy 1195 AAAAATGCTAACATC-ATTGAGCATTGAGTGAGTTGTAATCTTTTGGTGGTGAAGG 1253
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Qy 2503 AAAAATGCTGATTATCAATCTGAGCCCTCGGTGAGTCGTAATCTTTTGGTGGAGGG 2444
Db      |||||
Qy 1254 TCTTTTCTTATTGATGACTGAT-----CGGGGGTCAGGTGCTGAGGCTTAGGTT 1302
Db      |||||

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2323	Db	CTTTTCATGAAGATTTCTCTGTAGCATGCGATGCTGTTTGATAGCATTTTGGCCACAGTA	2264
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RESULT 15						
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DEFINITION	Homo sapiens BAC clone CTD-2005A22 from 4,				complete sequence.	
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VERSION	AC108017.4	GI:19526131				
KEYWORDS	HTG.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					

REFERENCE
mammalia; eutheria; primates; catarrhini; hominidae; homo.
1 (bases 1 to 51343)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
PUBMED 9847074

04/14/02

REFERENCE 2 (bases 1 to 51343)
AUTHORS Trani, L., Kozlowski, A. and Dignan, G.
TITLE The sequence of Homo sapiens BAC clone CTD-2005A22
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 51343)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE	4	(Bases 1 to 51343)	
AUTHORS		Waterston,R.H.	
TITLE		Direct Submission	
JOURNAL		Submitted (23-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	
REFERENCE	5	(Bases 1 to 51343)	
AUTHORS		Waterston,R.H.	
TITLE		Direct Submission	
JOURNAL		Submitted (16-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	
REFERENCE	6	(Bases 1 to 51343)	

AUTHORS	Waterston, R.
TITLE	Direct Submission
JOURNAL	Submitted (27-VAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT	On Mar 15, 2002 this sequence version replaced gi:18873881.

----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@wason.wustl.edu
----- Summary Statistics

Center project name: H MS2005A22

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence

from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

Clone CTD-2005A22 is from a release of the human BAC library CTD. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:18794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (<http://www.resgen.com>).

VECTOR: pBelO_{BAC}11
selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-719W18, 2000 bp overlap; the clone sequenced to the right is RP11-575B4, 2000 bp overlap. Actual start of this clone is at base position 120807 of RP11-719W18; actual end is at base position 7921 of RP11-575B4.

Polymorphisms have been identified between AC108017 and AC019341.

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